

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:40:11 ; Search time 12 Seconds
(without alignments)
1050.081 Million cell updates/sec

Title: US-10-068-564-5

Perfect score: 1239
Sequence: 1 MSNPRSLSEEEKYDMSGALTA.....KARKNPEIOSTLRKRYLYIQ 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1234	99.6	242	1	ICB6_HUMAN
2	934.5	75.4	257	1	ICB6_MOUSE
3	305	24.6	424	1	ICB2_CHICK
4	295	23.8	435	1	ICB2_MOUSE
5	289	23.3	435	1	ICB2_HUMAN
6	279.5	22.6	277	1	ICB3_RAT
7	277.5	22.4	277	1	ICB3_CRLO
8	273.5	22.1	277	1	ICB3_MOUSE
9	272.5	22.0	277	1	ICB3_HUMAN
10	270	21.8	303	1	ICB7_MOUSE
11	260	21.0	303	1	ICB7_MESAU
12	256	20.7	303	1	ICB7_HUMAN
13	248.5	20.1	503	1	ICB3_MOUSE
14	247.5	20.0	339	1	ICB3_MOUSE
15	246.5	19.9	479	1	ICB8_HUMAN
16	245	19.8	496	1	ICB8_MOUSE
17	240.5	19.4	276	1	ICB6_MOUSE
18	239.5	19.3	299	1	ICB6_HUMAN
19	237.5	19.2	416	1	ICB1_MOUSE
20	236.5	19.1	404	1	ICB1_MOUSE
21	233	18.8	480	1	ICB8_MOUSE
22	227	18.3	282	1	ICB3_XENLA
23	226.5	18.3	382	1	ICB8_XENLA
24	226	18.2	404	1	ICB3_HUMAN
25	225.5	18.2	323	1	ICB1_MOUSE
26	225	18.2	418	1	ICB5_HUMAN
27	222.5	18.0	386	1	ICB5_XENLA
28	222	17.9	293	1	ICB6_HUMAN
29	221.5	17.9	521	1	ICB6_HUMAN
30	218.5	17.6	402	1	ICB3_RAT
31	218	17.6	373	1	ICB4_MOUSE
32	217.5	17.6	402	1	ICB3_MOUSE
33	213.5	17.2	312	1	ICB2_RAT

34	212.5	17.2	405	1	ICB3_HUMAN
35	211	17.0	410	1	ICB3_MOUSE
36	209	16.9	404	1	ICB3_MOUSE
37	205.5	16.6	377	1	ICB4_HUMAN
38	196	15.8	377	1	ICB4_BOVIN
39	193.5	15.6	419	1	ICB3_MOUSE
40	194.5	15.4	484	1	ICB3_MOUSE
41	97	7.8	1051	1	APSB_EMBL
42	96	7.7	527	1	CSF2_ESRM
43	95.5	7.7	862	1	CSF2_MACR
44	95.5	7.7	2104	1	MYS3_SCHPO
45	94	7.6	480	1	CFIA_HUMAN

ALIGNMENTS

RESULT 1
ICB6_HUMAN STANDARD; PRT; 242 AA.
ID ICB6_HUMAN
AC P31944; 095823; (Rel. 26, Created)
DT 01-JUL-1993
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14).
GN CASP14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22168928; PubMed=12181750;
RA Picirito G., Jost M., Srinivasula S.M., Baffa R., Poyet J.-L.,
RA Kari C., Lazebnik Y., Rodeck U., Alnemri E.S.;
RT "Expression and transcriptional regulation of caspase-14 in simple
RT and complex epithelia."
RL Cell Death Differ. 9:995-1006(2002).
[2]
RP SEQUENCE OF 68-74; 137-147 AND 154-162.
RC TISSUE=Keratinocytes;
RX MEDLINE=93162043; PubMed=1266667;
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes."
RL Electrophoresis 13:960-969(1992).
CC -FUNCTION: May be involved in the death receptor and granzyme B
CC apoptotic pathways. May function as a downstream signal transducer
CC of cell death.
CC -SUBUNIT: May dimerize with large prodomain caspases.
CC -SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -SIMILARITY: Belongs to peptidase family C14.
CC
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CC
CC EMBL; AF097874; AAD16173.1; -
CC PIR; J07517; J07517.
CC HSSP; P29466; 1ICE.
CC Aarbus/Chent-2DPAGE; 6109; IEF.
CC MEROPS; C14.018; -
CC Genew; HGNC:1502; CASP14.
CC MIM; 605848; -
CC GO; GO:0004199; F: caspase activity; TAS.
CC GO; GO:0008544; P: epidermal differentiation; TAS.
CC InterPro; IPR002138; ICE_p10.

DR InterPro; IPR001309; ICE p20.
 DR InterPro; IPR002398; Peptidase C14.
 DR Pfam; PF00656; Peptidase C14; 1.
 DR PRINTS; PR00376; IL1BCENZYM.
 DR SMART; SM00115; CASc; 1.
 DR PROSITE; PS01121; CASPASE_HIS; FALSE_NEG.
 DR PROSITE; PS01122; CASPASE_CYS; FALSE_NEG.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR Hydrolyase; Thiol protease; Apoptosis; Zymogen.
 FT CHAIN 1 146
 FT CHAIN 147 242
 FT ACT_SITE 89
 FT ACT_SITE 132 132
 FT ACT_SITE 242 AA; 27679 MW; ES39PB78BD080A2 CRC64;
 SQ SEQUENCE

Query Match 99.6%; Score 1234; DB 1; Length 242;
 Best Local Similarity 99.6%; Pred. No. 5.8e-92;
 Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDLHMFROA PESTMKRDPPTAQ 60
 Db 1 MSNPRSLSEEEKYDMSGARLILCVTKAREGSEEDLDLHMFROA PESTMKRDPPTAQ 60
 QY 61 FOEELERFOQALIDREDPVSCAFVLMAGREGFLKGEDEGVKLLENLFEALNNKNCAL 120
 Db 61 FOEELERFOQALIDREDPVSCAFVLMAGREGFLKGEDEGVKLLENLFEALNNKNCAL 120
 QY 121 RAKPKVYIIQACREGEQDPGRTVWIKDSQPTITTYTDAHVSTVEGYIAYRH 180
 Db 121 RAKPKVYIIQACREGEQDPGRTVWIKDSQPTITTYTDAHVSTVEGYIAYRH 180
 QY 181 DQKGSCEIQTLDVVFTRKGHILELTVTRRMAEALVOEGARKNPICSTLRKRLY 240
 Db 181 DQKGSCEIQTLDVVFTRKGHILELTVTRRMAEALVOEGARKNPICSTLRKRLY 240
 QY 241 LQ 242
 Db 241 LQ 242

RESULT 2
 ICEE MOUSE STANDARD; PRT; 257 AA.
 AC 089094;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14) (MICE).
 GN CASP14.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=99040667; PubMed=9823333;
 RA Ahmad M., Srinivasula S.M., Hegde R., Mukattash R.,
 RA Fernandes-Alnemri T., Alnemri E.S.,
 RT "Identification and characterization of murine caspase-14, a new
 member of the caspase family.";
 RL Cancer Res. 58:5201-5205(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Embryo;
 RX MEDLINE=99222069; PubMed=10203698;
 RA Van den Craen M., Van Loo G., Pype S., Van Criekinge W.,
 RA Vandenabeele P.,
 RT "Identification of a new caspase homologue: caspase-14.";
 RL Cell Death Differ. 5:838-846(1998).

RM [3]
 RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-136.
 RX MEDLINE=99009076; PubMed=9792675;
 RA Hu S., Snipas S.J., Vincenz C., Salvesen G., Dixit V.M.,
 RT "Caspase-14 is a novel developmentally regulated protease.";
 RL J. Biol. Chem. 273:29648-29653(1998).
 CC -1- FUNCTION: Seems to be involved in the death receptor and granzyme
 B apoptotic pathways. May function as a downstream signal
 transducer of cell death. May play a role in ontogenesis and skin
 physiology.
 CC -1- SUBUNIT: May dimerize with large prodomain caspases.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
 CC -1- TISSUE SPECIFICITY: Embryo, adult liver and less in adult brain
 and kidney.
 CC -1- PTM: CLEAVAGE BY GRANZYME B, CASPASE-8 AND -10 GENERATES THE
 TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 PROTEASE.
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -----
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DR EMBL; AF092997; AAC6364.1; -;
 DR EMBL; AJ007750; CA07678.1; -;
 DR HSSP; P29466; 1ICE.
 DR MEROPS; C14.018; -;
 DR MED; MG1.1335092; Casp14.
 DR GO; GO:0006917; P:induction of apoptosis; IDA.
 DR InterPro; IPR002138; ICE p10.
 DR InterPro; IPR001309; ICE p20.
 DR InterPro; IPR002398; Peptidase C14.
 DR Pfam; PF00656; Peptidase C14; 1.
 DR PRINTS; PR00376; IL1BCENZYM.
 DR SMART; SM00115; CASc; 1.
 DR PROSITE; PS01121; CASPASE_HIS; FALSE_NEG.
 DR PROSITE; PS01122; CASPASE_CYS; FALSE_NEG.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR Hydrolyase; Thiol protease; Apoptosis; Zymogen.
 FT CHAIN 1 8
 FT CHAIN 2 257
 FT ACT_SITE 93 93
 FT ACT_SITE 136 136
 FT ACT_SITE 136 136
 FT MUTAGEN C->A: DECREASE IN DEATH-INDUCING
 ACTIVITY.
 SQ SEQUENCE 257 AA; 29458 MW; A228D8BDPFA0B84 CRC64;

Query Match 75.4%; Score 934.5; DB 1; Length 257;
 Best Local Similarity 70.9%; Pred. No. 6.5e-68;
 Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;

QY 1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDLHMFROA PESTMKRDPPTAQ 60
 Db 5 MSNPRSLSEEEKYDMSGARLILCVTKAREGSEEDLDLHMFROA PESTMKRDPPTAQ 60
 QY 61 FOEELERFOQALIDREDPVSCAFVLMAGREGFLKGEDEGVKLLENLFEALNNKNCAL 120
 Db 65 FOEELERFOQALIDREDPVSCAFVLMAGREGFLKGEDEGVKLLENLFEALNNKNCAL 124
 QY 121 RAKPKVYIIQACREGEQDPGRTVWIKDSQPTITTYTDAHVSTVEGYIAYRH 168
 Db 125 RAKPKVYIIQACREGEQDPGRTVWIKDSQPTITTYTDAHVSTVEGYIAYRH 183
 QY 169 YSTVEGYIAYRHDPKGSCEIQTLDVVFTRKGHILELTVTRRMAEALVOEGARKNPICSTLRKRLY 228
 Db 184 YSTVEGYIAYRHDPKGSCEIQTLDVVFTRKGHILELTVTRRMAEALVOEGARKNPICSTLRKRLY 243

OY	229	PELOSTIKRKYLO	242
		: : : : : :	
D6	244	PEVOSTIKRKLYLO	257

RESULT 3			
ID	_ICE2_CHICK	STANDARD;	PRT; 424 AA.
AC	Q98943;		
DT	01-NOV-1997	(Rel. 35, Created)	
DT	01-NOV-1997	(Rel. 35, Last sequence update)	
DT	10-OCT-2003	(Rel. 42, Last annotation update)	
DE	Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-1L/1S).		
GN	CASP2 OR ICH1.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
CC	Gallus.		
CC	NCBI_TaxID=9031;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORMS ICH-1L AND ICH-1S).		
RC	STRAIN=White Leghorn; TISSUE=Ovarian granulosa;		
RC	MEDLINE=97368127; Pubmed=9224894;		
RA	Johnson A.L., Birdgham J.T., Bergeron L., Yuan J.;		
RT	"Characterization of the avian Ich-1 cDNA and expression of Ich-1L mRNA in the hen ovary";		
RL	Gene 192:227-233(1997).		
CC	-I- FUNCTION: Involved in the activation cascade of caspases responsible for apoptosis execution. Might function by either activating some proteins required for cell death or inactivating proteins necessary for cell survival (By similarity).		
CC	-I- ALTERNATIVE PRODUCTS:		
CC	Event=Alternative splicing; Named isoforms=2;		
CC	Name=ICH-1L;		
CC	IsoId=Q98943-1; Sequence=Displayed;		
CC	Note=Only form found in the ovary;		
CC	Name=ICH-1S;		
CC	IsoId=Q98943-2; Sequence=VSP_000803, VSP_000804;		
CC	-I- PTM: Heterodimer of a small and a large subunit (By similarity).		
CC	-I- SIMILARITY: Belongs to peptidase family C14.		
CC	-I- SIMILARITY: Contains 1 CARD domain.		
CC	-----		
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CC	-----		
DR	EMBL, U64963; AAC29881.1; ALT_INIT.		
DR	HSSP; P42574; ICPI3.		
DR	MEROBS; C14_006; -.		
DR	InterPro: IPRO01315; CARD.		
DR	InterPro: IPRO02138; ICE_P10.		
DR	InterPro: IPRO01309; ICE_P20.		
DR	InterPro: IPRO02398; Peptidase_C14.		
DR	Pfam; PF00619; CARD; 1.		
DR	Pfam; PF00656; Peptidase_C14; 1.		
DR	PRINTS; PR00376; IL1BCENZME.		
DR	SMART; SMO0114; CARD; 1.		
DR	SMART; SMO0115; CASC; 1.		
DR	PROSITE; PS50209; CARD; 1.		
DR	PROSITE; PS01122; CASPASE_CY2; 1.		
DR	PROSITE; PS01121; CASPASE_HIS; 1.		
DR	PROSITE; PS50207; CASPASE_P10; 1.		
KW	PROSITE; PS50208; CASPASE_P20; 1.		
FT	Hydrolase; Thiol protease; Apoptosis; Zymogen; Alternative splicing.		
FT	PROPEP 1		
FT	CHAIN 141		
FT	CHAIN 309		
FT	CHAIN 424		
FT	CASPASE-2 SUBUNIT P18 (BY SIMILARITY).		
FT	CASPASE-2 SUBUNIT P13 (BY SIMILARITY).		

FT	CHAIN	315	424	96	CASPASE-2 SUBUNIT P12 (BY SIMILARITY).
FT	DOMAIN	7	96		CASP.
FT	ACT SITE	248	248		BY SIMILARITY.
FT	ACT SITE	291	291		BY SIMILARITY.
FT	WASAPLIC	1	7		Missing (in isoform ICH-1S).
FT	VARAPLIC	294	424		/FTId=VSP 000803.
FT					DETROGVDORGRKSRDSPGCEESDANKENIKLPTFRSD
FT					MICGYALCKLGTGAARNRNTKRGSWYETALTTVAEDSRDTHVA
FT					DMLVKVRNQLKOREGYAPGTEFHRCKEMSEVCTLCRDLYL
FT					PEGVVPGK -> GVSGLIHILPLPCCHCICICSMRQISEMI
FT					REMAKNGQIPQAVRRVMQTRKXIKSSVCGLHAPI (in
FT					isoform ICH-1S).
FT					/FTId=VSP 000804.
SEQ	SEQUENCE	424 AA;	47959 MW;	722810508B8B2F60 CRC64;	
	Query Match	24.6%;	Score 305;	DB 1;	Length 424;
	Best Local Similarity	31.5%;	Pred. No. 3.7e-17;		
	Matches	86;	Conservative	51;	Mismatches 82;
					Indels 54;
					Gaps 10;
QY		1	MSNPRLSEEEKYDMSGALAILLC-----VTKAREGSEEDDIALEHMPLQALFEESTM	52	
DB		166	ISEPP-----GIALILINIHSESEKDELYRSGVDVDCASLELFFHILGQYTV	213	
QY		53	KDPTFAHQFOEELKEFQOALISREDPVSCAFVYLMARREGFLKDEDEMYLLENLFEAL	112	
DB		214	FHDQSAEENESALBERFSKLPD-HQVVDSC-IYALSHVEGVGVTGDLTQLQLEAFRLF	271	
QY		113	NNKNQCALRAKPKYVYIIQAQCRGEQRPDQ-ETVYGDELYWVYKDS-----Q	157	
DB		272	DVANCENLIKQNKXKMFELIQAQCRGDEIDTRDGVDRQDKE---RSDSPCEESDANKENKLT	327	
QY		158	TIPTYTDAIAVSYVEGYIAVHHQDQSGEFTQIVDVETK--RKGHILELLETVTRMAE	215	
DB		328	RLPTSDMIGCYAGLKTGAAMNTRKGSYVIALTTVEAEDSRDLTHVADMLVKNRQIQ	387	
QY		216	AEVYDQSKARKTN-----PEIOSYTLRRLYV	241	
DB		388	---REGVAPGTEFHRCKEMSEYCSITLCDVLI	416	
RESULT 4					
ICE2	MOUSE		STANDARD;	PRT;	435 AA.
ID	ICE2_MOUSE				
AC	P29594;	008737;			
DT	01-APR-1993	(Rel. 25, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	15-MAR-2004	(Rel. 43, Last annotation update)			
DE	Caspase-2 precursor (BC 3.4.22.-) (CASP-2) (ICH-1 protease) (NEDD2				
DS	protein).				
OS	CASP2 OR ICH1 OR NEDD2 OR NEDD-2.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
NP	[1]				
NP	SEQUENCE FROM N.A.				
RC	STRAIN=BALB/c;				
RX	MEDLINE=95047319;	PubMed=7958843;			
RA	Kumar S., Kinoshita M., Noda M., Copeland N.G., Jenkins N.A.;				
RT	"Induction of apoptosis by the mouse Nedd2 gene, which encodes a				
RT	protein similar to the product of the Caenorhabditis elegans cell				
RT	death gene ced-3 and the mammalian IL-1 beta-converting enzyme.";				
RL	Genes Dev. 8:1613-1626(1994).				
RM	[2]				
RM	SEQUENCE FROM N.A.				
RC	STRAIN=C3H/An;				
RX	MEDLINE=97190206;	PubMed=9038361;			
RA	van de Crien M., Vandenaebelle P., Declercq W., van den Brande I.,				
RA	van Looy G., Molemans F., Schotte P., van Crielinge W., Beyaert R.,				
RA	Fiers W.;				
RT	"Characterization of seven murine caspase family members.";				
RL	FEBS Lett. 403:61-69(1997).				
RN	[3]				

RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
RC TISSUE=Brain:
RA MEDLINE=92328780; PubMed=1378265;
RX Kumar S., Tomooka Y., Noda M.;
RT "Identification of a set of genes with developmentally down-regulated
RL expression in the mouse brain.";
RL Blochm. Biophys. Res. Commun. 185:1155-1161(1992).
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Might function by either
CC activating some proteins required for cell death or inactivating
CC proteins necessary for cell survival. May be important in
CC multistep carcinogenesis.
CC
CC -1- SUBUNIT: Heterodimer of a small and a large subunit (By
CC similarity).
CC
CC -1- TISSUE SPECIFICITY: High level expression seen in the embryonic
CC CNS, liver, lung, kidney, small intestine, and hair follicles of
CC vibrissae. Moderate expression seen in the skin, oral mucosa,
CC skeletal muscle, submandibular gland and thymus. In the adult, it
CC is highly expressed in spleen, lung and kidney. Moderately in the
CC brain, heart, testis, liver. Low levels in the thymus, skeletal
CC muscle, ovary and gut.
CC
CC -1- DEVELOPMENTAL STAGE: During embryonic development is highly
CC expressed in several types of mouse tissue undergoing high rates
CC of programmed cell death such as central nervous system and
CC kidney.
CC
CC -1- PTM: THE NATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
CC THAT OF OTHER CASPASES (BY SIMILARITY).
CC
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC
CC -1- SIMILARITY: Contains 1 CARD domain.
CC
CC -----
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CC -----
DR EMBL, D28492; BAA25876.1; ALT_INIT.
DR EMBL, Y13085; CAA73527.1; ALT_INIT.
DR HSSP; P42574; IC93.
DR MEROPS; C14.006; -.
DR MGD; MGI:97295; Casp2.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILLIBENZYM.
DR SMART; SMO0114; CARD; 1.
DR SMART; SMO0115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR Hydrolyase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 152
FT CHAIN 152
FT CHAIN 153
FT CHAIN 316
FT CHAIN 317 435
FT CHAIN 331 435
FT CHAIN 15 103
FT DOMAIN 15 103
FT ACT_SITE 260 260
FT ACT_SITE 303 303
FT ACT_SITE 303 303
FT MUTAGEN 303 303
FT COMPACT 71 71
SQ SEQUENCE 435 AA; 48896 MW; 8984E6AA76E7A676 CRC64;
MISSING (IN REF. 1).

Qy	29	RESSESDDLALEHMFQARESTMKDPDTAECQOELEKFKQQAIDSRBDPSCAFVVLMA	140
Db	202	RSGGDVDDHTTLVTLLFKLLGNVAVHLDQTAQOEKQLONFAQ-LTPAHRYVDSCV-VALLS	259
Qy	89	HGHEGLFKGDEGMVTKLEMLFEALNNKNCOALPAKPKVYVIOACREGRDPRG-----	140
Db	260	HGVEGGIYGVDDGLLDLQGEVFRLEFDANCSLQNKRFMEFTQACRGDETRGVQDQDGN	319
Qy	141	-----FTVGDEIVVYIKDSPQTIPPTVYALAHVYSTVEGYIANYHDQGSCEIOTLV	132
Db	320	HTQSPCCESDPAQKEELMKMR-----LTPRSDMIGVACLKGAAMNTRGSGWYIALT	374
Qy	193	DVFTRK-KGHLELLEITYTRMAEALVQEGARKTN-----PEIQSTLRRLYL	241
Db	375	QVFSERACMHEVADMLVKVALIKE---REGYAPETEPHRCRESEYCSLLQOYL	428
RESULT 5			
ICB2_HUMAN			
ID	ICE2_HUMAN	STANDARD;	PRT; 435 AA.
AC	P42575; P42576;		
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-1L1S)		
GN	CASP2 OR ICH1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).		
RC	TISSUE=Fetal brain;		
RA	MEDLINE=94373811; PubMed=8087842;		
RT	Wang L., Miura M., Bergeron L., Zhu H., Yuan J.;		
RT	"Ich-1, an Ice/Ced-3-related gene, encodes both positive and negative		
RL	Cell 78:739-750(1994).		
RN	[2]		
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS LEU-155; ATA-161 AND		
RA	GLY-424.		
RT	Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,		
RA	Miyamoto K.E., Nguyen C.P., Nguyen D.A., Peol C.L., Robertson P.D.,		
RA	Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;		
RL	Submitted (VAN-2003) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RA	Doebber A., Martinka S., Maupin R.;		
RL	Submitted (GUN-2000) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	CLEAVAGE SITES.		
RX	MEDLINE=96206041; PubMed=8654923;		
RA	Xue D., Shahan S., Horvitz H.R.;		
RT	"The Caenorhabditis elegans cell-death protein CED-3 is a cysteine		
RT	protease with substrate specificities similar to those of the human		
RT	CPP32 protease."		
RL	Genes Dev. 10:1073-1083(1996).		
CC	-1- FUNCTION: Involved in the activation cascade of caspases		
CC	responsible for apoptosis execution. Might function by either		
CC	activating some proteins required for cell death or inactivating		
CC	proteins necessary for cell survival.		
CC	-1- SUBUNIT: Heterodimer of a small and a large subunit (By		
CC	similarity).		
CC	-1- ALTERNATIVE PRODUCTS:		
CC	Event=Alternative splicing; Named isoforms=2;		
CC	Comment=Isoforms differ in the N- and C-terminal;		
CC	Name=ICH-1L;		
CC	isoId=P42575-1; Sequence=Displayed;		
CC	Note=Acts as a positive regulator of apoptosis;		
CC	Name=ICH-1S;		
CC	isoId=P42575-2; Sequence=VSP_000801, VSP_000802;		
CC	Note=Acts as a negative regulator of apoptosis;		
CC			

CC -1- TISSUE SPECIFICITY: Expressed in larger amounts in the embryonic
CC lung, liver and kidney than in the heart and brain. In the adults
CC higher level expression is seen in the placenta, lung, kidney,
CC pancreas than in the heart, brain, liver and skeletal muscle.
CC -1- PFM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
CC THAT OF OTHER CASPASES.
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U13021; AA58959.1; -;
CC EMBL; U13022; AA58960.1; -;
CC EMBL; AY219042; AA025653.1; -;
CC EMBL; AC073342; AAP2346.1; -;
CC PIR; A54821; A54821.
CC HSSP; P29466; 1ICE.
CC MEROPS; C14.006; -;
CC Genew; HGNC:1503; CASP2.
CC MIM; 600639; -;
CC GO; GO:0004202; F:caspase-2 activity; TAS.
CC GO; GO:0018999; F:enzyme binding; ISS.
CC GO; GO:0008632; P:apoptotic program; TAS.
CC GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
CC InterPro; IPR001315; CARD.
CC InterPro; IPR002138; ICE p10.
CC InterPro; IPR001309; ICE p20.
CC InterPro; IPR002398; Peptidase_C14.
CC Pfam; PF00619; CARD; 1.
CC Pfam; PF00656; Peptidase_C14; 1.
CC PRINTS; PR00376; ILIBCEZYME.
CC SMART; SM00114; CARD; 1.
CC SMART; SM00115; CASG; 1.
CC PROSITE; PS50209; CARD; 1.
CC PROSITE; PS01122; CASPASE_CYS; 1.
CC PROSITE; PS01121; CASPASE_HIS; 1.
CC PROSITE; PS50207; CASPASE_P10; 1.
CC PROSITE; PS50208; CASPASE_P20; 1.
CC K0 Hydroxylase; Thiol protease; Apoptosis; Zymogen; Polymorphism;
KW Alternative splicing
FT PROPEP 1 152
FT CHAIN 153 308 CASPASE-2 SUBUNIT P18.
FT PROPEP 309 316
FT CHAIN 317 435 CASPASE-2 SUBUNIT P13.
FT CHAIN 331 435 CASPASE-2 SUBUNIT P12.
FT DOMAIN 15 103 CARD.
FT ACT_SITE 260 260 BY SIMILARITY.
FT ACT_SITE 303 303 BY SIMILARITY.
FT VARSPIC 1 14 Missing (in isoform ICH-1S).
FT VARSPIC 306 435 /FTid=VSP_000801.
FT DETRGVDDGKXNHASPGCEESDAGEKELPKRLPTRSD
FT MCGYACIKGTAAKNTKRGVTEALAOVSEKACMHTVA
FT DMUYKVALITKDRGVAPGTFEHHCKMSEVCSITLCHLYL
FT FPGHPT -> GAIIGSIGHLLTFAATASIAL (in
FT isoform ICH-1S).
FT /FTid=VSP_000802.
FT V -> L.
FT /FTid=VSP_016334.
FT P -> A.
FT /FTid=VAR_016335.
FT VARIANT 155 155
FT VARIANT 161 161
FT VARIANT 424 424
FT VARIANT 424 424
FT MUTAGEN 303 303 R -> G.
FT MUTAGEN 352 352 C -> S; LOSS OF FUNCTION.
FT SEQUENCE 435 AA; 48855 MM; 1652EC73FE286FB7 CRC64;
Query Match 23.3%; Score 289; DB 1; Length 435;

Best Local Similarity 31.1%; Pred. No. 7.3e-16;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;
QY 29 REGSEDLALHEHFRQLRFESTKAPPTAQQPBELEKFOQALDSKEDPVCAPVYMA 88
DB 202 RSGDVHSTLVTLFKLLGVDVHVLCDQTAEMERKQNFQAQ-IPARVTDSC-IVALLS 259
QY 89 HGRGFLKGEHGEVWVKNLEFELNKKCCALRAKPKVYIIOACRGEDRDPG----- 140
DB 260 HGVEGALYGVGDKLQLOEVFOLFDNANCPSELQNKPKRFIOACRGEDTDKGVDDGDKN 319
QY 141 -----ETVGGDEIVWVIXDSPTIPTYDALHVSTVEGYIAYRHQKSCFTIQLY 192
DB 320 HAGSGCEESDAGE-----KLPPKRLPTRSDMTCGVACLKGTAAKRTKGSWYTEALIA 374
QY 193 DVFTKR--KGHLELITVETRMADAEVQSKARKTN-----PEQSTLRKRYL 241
DB 375 QVFSERACDMHVADMLVKNALIKD---RGGYAGTEFFHCKMKSEVCSITLCHLYL 428
RESULT 6
ID ICE3 RAT STANDARD; PRT: 277 AA.
AC P55213; P70543; P97699; Q62993;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptain precursor (BC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CPP-32) (Caspase-3) (SREBP cleavage activity 1)
DE (SCA-1) (LICE) (TRP).
GN CASP3 OR CPP32.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96358624; PubMed=8761296;
RA Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
RA Fletcher F.A.;
RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
RT a cysteine protease resembling interleukin-1 beta converting enzyme
RT and CED-3.";
RL Oncogene 13:749-755 (1996).
RN [2]
RP SEQUENCE OF 30-241 FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=96042508; PubMed=7588240;
RA Plaws J.A., Kugu K., Trbovich A.M., Desanti A., Tilly K.I.,
RA Hirschfield A.N., Tilly J.L.;
RT "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and
RT mammalian cell death: dissociation of IRP-induced oligonucleosomal
RT endonuclease activity from morphological apoptosis in granulosa cells
RT of the ovarian follicle.";
RL Endocrinology 136:5042-5053 (1995).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97184204; PubMed=9030616;
RA Ni B., Wu X., Du Y., Su Y., Hamilton-Byrd E., Rockey P.K.,
RA Roelcke P., Jr., Polier G.G., Paul S.M.;
RT "Cloning and expression of a rat brain interleukin-1beta-converting
RT enzyme (ICE)-related protease (IRP) and its possible role in
RT apoptosis of cultured cerebellar granule neurons.";
RL J. Neurosci. 17:1561-1569 (1997).
RN [4]
RP SEQUENCE OF 1-264 FROM N.A.
RA Yakovlev A.G.;
RC Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. At the onset of apoptosis it
CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
CC 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory

```

Db      94  EIMELINDSVKREHSHKRSKSSFCV--VILSHGDEGVIFGNGP-VDLKULTSPFRGDCYR 149
Qy      119 ALRAKPKYITIIQACRGGRDPFG-ETVGGDEIIVWIKDSPQITPIYTTALHVSSTVEGYIA 177
Db      150 SLTKPKPLFIIOACRGTELDGIEFTSDGTDMMAC-----OKIPEADFLVANSIAPGIYS 205
Qy      178 YRHOKSCSCFQTVVDVFTYRKHIIE---LLEVTETRA---EAEIYOGKARKTNP 236
Db      206 WRNSRDSQSWFLQSTQ-C-AMLKLYAKFLKEFMHILTVRNKRVAETEFESFLDPTFAKKQIIPC 265
Qy      231 IOSTLRKRLY 240
Db      265 IVSYLTKELY 274

RESULT 7
ICE3 CRIL0
ID ICE3 CRIL0 STANDARD; PRT; 277 AA.
AC 060431;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Abpman precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
(SCA-1).
GN CASP3 OR CPP32.
OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OX Cricetulus.
NC NCB1_Taxid=10030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=9618185; PubMed=8605870;
RA Mang X., Zelemski N.G., Yang J., Sakai J., Brown M.S.,
RA Goldstein J.L.;
RT "Cleavage of sterol regulatory element binding proteins (SREBPs) by
RT CPP32 during apoptosis."
RL EMO J. 15:1012-1020(1996).
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. At the onset of apoptosis it
CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
CC 216-Asp-1-Gly-217 bond. Cleaves and activates sterol regulatory
CC element binding proteins (SREBPs) between the basic helix-loop-
CC helix leucine zipper domain and the membrane attachment domain.
CC Cleaves and activates caspase-6, -7 and -9 (By similarity).
CC -!- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
CC VICE VERSA (BY SIMILARITY).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC -----
DR EMBL; U27463; AB01511.1; -.
DR HSSP; P42574; IPAU.
DR MEROPS; C14.003; -.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase C14; 1.

```

PRINTS: PR00376; IILBCNZYME.
 DR SMART: SMO0115; CASP: 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 KW Hydrolyase; Thiol protease; Zymogen; Apoptosis.
 FT PROPEP 1 9
 FT CHAIN 10 28
 FT CHAIN 29 175
 FT ACCT SITE 121 121
 FT ACCT SITE 163 163
 FT ACCT SITE 163 163
 SEQUENCE 277 AA; 31612 MW; 0BF3A4590A2828A3 CRC64;
 Query Match 22.4%; Score 277.5; DB 1; Length 277;
 Best Local Similarity 35.9%; Pred. No. 3,4e-15;
 Matches 79; Conservative 31; Mismatches 93; Indels 17; Gaps 7;
 QY REGSEDDDALEHMFROIRFESTMKRDPFAEQFOELEKFOQALIDREDPVSCAFVDMA 88
 DB 64 RSGTVDAKLRKERTMALKYEVKKNLDIREIVELMKNAKEDSKSSFC--VILS 120
 QY HGRSEGLKGEDEGVYLTENLFEALNNKNCQALRARKVYIIQACRGEQDPG-ETVGGDE 147
 DB 121 HDDEGVITFTDGP-IDKKTLYTFREDYCRSLIGKPKLIIOACRGTEIDCGIETDSGTE 179
 QY 148 IYMWIKDSPTPTPTDIAHYSTVEGYIAYRHDKGSGEIQTLVDVFKRGHILE--- 204
 DB 180 DDMTC---QKIPVEADFLYAVSTAGYISMRPKDGSWFISLSCML-KLYAHKLEFWM 234
 QY 205 ILTEVTRMA---EALVQEGKARKTNPEIOSTLEKRLY 240
 DB 235 ILFRNKKVATREFESLDSSTPHAKQICIVSMILKELY 274

RESULT 8
 IC33 MOUSE STANDARD; PRT; 277 AA.
 ID IC33_MOUSE
 AC P70677; O08668; Q9QW14;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptin precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1) (SCA-1) (LICE).
 GN CASP3 OR CPP32.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96358624; PubMed=8761296;
 RA Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G., Fletcher P.A.;
 RT "Molecular characterization of mouse and rat CPP32 beta gene encoding a cysteine protease resembling interleukin-1 beta converting enzyme and CBD-3.";
 RT Oncogene 13:749-755 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97224429; PubMed=9070890;
 RA Mukasa T., Urase K., Momoi M.Y., Kimura I., Momoi T.;
 RT "Specific expression of CPP32 in sensory neurons of mouse embryos and activation of CPP32 in the apoptosis induced by a withdrawal of NGF.";
 RT Biochem. Biophys. Res. Commun. 231:770-774 (1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C3H/An;
 RX MEDLINE=97190206; PubMed=9038361;
 RX van de Craen M., Vandenberghe P., Declercq W., van den Brande I.,

RA van Loo G., Molemans F., Schotte P., van Criekinge W., Beyaert R.,
 RA Fiers W.;
 RT "Characterization of seven murine caspase family members.";
 RL FEBS Lett. 403:61-69 (1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
 RL Submitted (May-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Ditchenko L., Marins K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein W.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Blakesley R.W., Touchman J.W., Schmitz J., Myers R.M.,
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [6]
 RP SEQUENCE OF 58-277 FROM N.A.
 RA Denis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O.,
 RA Fortin J.-P., Sekaly R.-P.;
 RT Submitted (Jul-1996) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. At the onset of apoptosis it
 CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
 CC 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory
 CC element binding proteins (SREBPs) between the basic helix-loop-
 CC helix leucine zipper domain and the membrane attachment domain.
 CC Cleaves and activates caspase-6, -7 and -9 (by similarity).
 CC cleaves IL-1 beta between an Asp and an Ala, releasing the mature
 CC cytokine which is involved in a variety of inflammatory processes.
 CC -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Highest expression in spleen, lung, liver,
 CC kidney and heart. Lower expression in brain, skeletal muscle and
 CC testis.
 CC -1- PTM: CLEAVAGE BY GRANTYME B, CASPASE-6, -8 AND -10 GENERATES THE
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC
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 CC
 CC EMBL; U54803; AAC52768.1; JOINED.
 CC EMBL; U54802; AAC52768.1; JOINED.
 CC EMBL; U49929; AAC52764.1; -

RL Nat. Struct. Biol. 3:619-625 (1996).
 [8]
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.
 RP MEDLINE=97197830; PubMed=9045680;
 RX Mittl P.R.E., di Marco S., Krebs J.F., Bai X., Katanewsky D.S.,
 RA Priestle J.P., Tomaselli K.J., Grueter M.G.,
 RT "Structure of recombinant human CPP32 in complex with the
 RT tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone";
 RL J. Biol. Chem. 272:6539-6547 (1997).
 [9]
 RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RP MEDLINE=20283632; PubMed=10821855;
 RX Lee D., Long S.A., Adams U.L., Chan G., Vaidya K.S., Francis T.A.,
 RA Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S.,
 RA Levy M.A., Dewolf W.E. Jr., Keller P.M., Tomaszek T., Head M.S.,
 RA Ryan M.D., Hattiwanger R.C., Liang P.-H., Janson C.A., McDevitt P.J.,
 RA Johnson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,
 RA Jack M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.,
 RT "Potent and selective nonpeptide inhibitors of caspases 3 and 7
 RT inhibit apoptosis and maintain cell functionality";
 RL J. Biol. Chem. 275:16007-16014 (2000).
 [10]
 RN PROCESSING.
 RP MEDLINE=96353838; PubMed=8755496;
 RX Fernandez-Alnemir T., Armstrong R.C., Krebs J., Srinivasula S.M.,
 RA Wang L., Bullrich F., Fritze L.C., Trapani J.A., Tomaselli K.J.,
 RA Litwack G., Alnemir E.S.,
 RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
 RT apoptotic cysteine protease containing two FADD-like domains";
 RT Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469 (1996).
 [11]
 RN CLEAVAGE OF HUNTINGTIN.
 RP MEDLINE=96331285; PubMed=8696339;
 RX Goldberg Y.P., Nicholson D.W., Rasper D.M., Kalchman M.A., Koide H.B.,
 RA Graham R.K., Brom M., Kazemi-Esfarjani P., Thornberry N.A.,
 RA Vallancourt J.P., Hayden M.R.,
 RT "Cleavage of huntingtin by apolipin, a proapoptotic cysteine protease,
 RT is modulated by the polyglutamine tract";
 RL Nat. Genet. 13:442-449 (1996).
 -1- FUNCTION: Involved in the activation cascade of caspases
 responsible for apoptosis execution. At the onset of apoptosis it
 proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
 216-Asp-1-gly-217 bond. Cleaves and activates sterol regulatory
 element binding proteins (SREBPs) between the basic helix-loop-
 helix leucine zipper domain and the membrane attachment domain.
 Cleaves and activates caspase-6, -7 and -9. Involved in the
 cleavage of huntingtin.
 -1- ENZYME REGULATION: Inhibited by isatin sulfonamides.
 -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit.
 -1- SUBCELLULAR LOCATION: Cytoplasmic.
 -1- TISSUE SPECIFICITY: Highly expressed in lung, spleen, heart, liver
 and kidney. Moderate levels in brain and skeletal muscle, and low
 in testis. Also found in many cell lines, highest expression in
 cells of the immune system.
 -1- PTM: CLEAVAGE BY GRANZYME B, APAF-1, CASPASE-6, -8 AND -10
 GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
 PROPERTIES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
 ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
 OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
 AND VICE VERSA.
 -1- SIMILARITY: Belongs to peptidase family C14.
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 CC or send an email to license@isb.ch).
 CC -----
 DR EMBL; U13737; AAA65015.1; -;
 DR EMBL; U13738; AAB60355.1; -;
 DR EMBL; U26943; AAA74929.1; -;

DR EMBL; A1413269; CAC88866.1; -;
 DR EMBL; AY199666; AA025654.1; -;
 DR EMBL; BC016926; AA016926.1; -;
 DR PIR; A53315; A53315.
 DR PIR; 1PAU; 07-JUL-97.
 DR PDB; 1CP3; 24-DEC-97.
 DR PDB; 1GFM; 23-JUN-00.
 DR MEROPS; C14.003; -;
 DR GeneW; HGNC:1504; CASP3.
 DR MIM; 600636; -;
 DR GO; GO:0004208; F:caspase-3 activity; TAS.
 DR GO; GO:0008624; P:induction of apoptosis by extracellular sig. .; TAS.
 DR GO; GO:0008629; P:induction of apoptosis by intracellular sig. .; TAS.
 DR GO; GO:0009405; P:pathogenesis; TAS.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR InterPro; IPR002398; Peptidase C14.
 DR Pfam; PF00656; Peptidase C14; 1.
 DR PRINTS; PR00376; IL1BCENZYM.
 DR SMART; SM00115; CASc; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS02027; CASPASE_P10; 1.
 DR PROSITE; PS02028; CASPASE_P20; 1.
 KW Hydrolase; Thiol protease; Zymogen; Apoptosis; Polymorphism;
 KW 3D-structure.
 FT PROPEP 1 9
 FT PROPEP 10 28
 FT CHAIN 29 175
 FT CHAIN 176 277
 FT ACT_SITE 121 121
 FT ACT_SITE 163 163
 FT VARIANT 190 190
 FT VARIANT 190 190
 FT CONFLICT 31 36
 FT STRAND 36 36
 FT STRAND 43 51
 FT HELIX 57 59
 FT TURN 60 60
 FT TURN 65 66
 FT TURN 67 80
 FT HELIX 81 82
 FT TURN 81 82
 Query Match 22.0%; Score 272.5; DB 1; Length 277;
 Best Local Similarity 31.9%; Pred. No. 8,7e-15;
 Matches 80; Conservative 39; Mismatches 103; Indels 29; Gaps 9;
 QY 9 EEEKYDMSGALALILCVTK-----AREGSEEDLALHEMFEROLRESMKDPTA 58
 DB 34 DNYKYDYPKMGCTIINNNGFHKSTGTSRSGTVDVDAIMRETFRLKYEVNRKNDLTR 93
 QY 59 EGFQELERKQQAIDREDEVSQAFVYLMHGRGELKGDG--EWVKLENTLFPALNNKN 116
 DB 94 EEIYELMRDVSKEHDSRSSSFCV--VLSHGEGGILFGTNGPVDLKKTINF--RGDR 147
 QY 117 GQLRAKPKYITDAGCEGDRPG--ETVSGDEIYVTKDSFQITPTYTDAIHYVSTVEGY 175
 DB 148 CRSLTGKPKFLIDACGTBIDGSLIFDTSQVDDMAC---HKIPVADFLVASTAPGY 203
 QY 176 IAYRHDKSGSCFTIOTLVDFTK--RKSHILELTVTRRNA--EELVYO--EGARKTNP 229
 DB 204 YSWNSNDGSGFISTGLCMLEKQYADKLEFMIILTRVVRKVAETEFSSPFDATFPAKOIP 263
 QY 230 EIGSTLKKRLY 240
 DB 264 CIVSMLTRELY 274
 RESULT 10
 ICE7 MOUSE STANDARD; PRT; 303 AA.
 ID ICE7 MOUSE
 AC P97864; C08669;
 DT 01-NOV-1997 (rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caspase-7 precursor (EC 3.4.22.-) (LICE2 cysteine protease) (Apoptotic
 GN protease Mch-3).
 OS CASP7 OR MCH3 OR LICE2.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skelletal muscle;
 RA MEDLINE=97224489; PubMed=9070923;
 RX Juan T.S.-C., Mchiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
 RA Copeland N.G., Fletcher F.A.;
 RT "Identification and mapping of Casp7, a cysteine protease resembling
 RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3.";
 RL Genomics 40:86-93 (1997).
 [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=97236307; PubMed=9125129;
 RA Mukasa T., Khorojy Y., Tsukahara T., Momoi M.Y., Kimura I.,
 RA Momoi T.;
 RT "Mortaminin enhances CPP32-like activity during neuronal
 RT differentiation of P19 embryonal carcinoma cells induced by retinoic
 RT acid.";
 RL Biochem. Biophys. Res. Commun. 232:192-197 (1997).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/An;
 RA MEDLINE=97190206; PubMed=9038361;
 RX van de Craen M., Vandenaebale P., Declercq W., van den Brande I.,
 RA Fiers W.;
 RT "Characterization of seven murine caspase family members.";
 RL FEBS Lett. 403:61-69 (1997).
 [4]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.U., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butcherfield Y.S.N., Krzywinski M.T., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [5]
 RP FUNCTION: Involved in the activation cascade of caspases
 responsible for apoptosis execution. Cleaves and activates sterol
 regulatory element binding proteins (SREBPs). Overexpression
 promotes programmed cell death (by similarity).
 [6]
 RP SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit.
 [7]
 RP SUBCELLULAR LOCATION: Cytoplasmic.
 [8]
 RP TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LUNG, LIVER, AND
 KIDNEY. LOW LEVELS IN SPLEEN, SKELETAL MUSCLE, AND TESTIS. NO
 EXPRESSION IN THE BRAIN.
 [9]
 RP PM: CLEAVAGES BY GRANTYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
 SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
 CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
 VICE VERSA (BY SIMILARITY).

CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -----
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 CC -----
 DR EMBL: U67321; AAC53068.1; ALT_INIT.
 DR EMBL: D86353; BAA19730.1; -.
 DR EMBL: Y13088; CAA73530.1; -.
 DR EMBL: BC005428; AAB05428.1; -.
 DR HSSP: P42574; 1PAU.
 DR MEROPS: C14.004; -.
 DR MCD: MGI:109383; Casp7.
 DR InterPro: IPR002138; ICE_P10.
 DR InterPro: IPR001309; ICE_P20.
 DR InterPro: IPR002398; Peptidase_C14.
 DR Pfam: PF00656; Peptidase_C14; 1.
 DR PRINTS: PR00376; IL1BCENZYM.
 DR SMART: SW00115; CASC; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 KW Hydrolase; Thiol protease; Zymogen; Apoptosis.
 FT PROPEP 1 23
 FT CHAIN 24 198
 FT PROPEP 199 206
 FT CHAIN 207 303
 FT ACT_SITE 144 144
 FT ACT_SITE 186 186
 FT CONFLICT 10 11
 FT CONFLICT 45 45
 FT CONFLICT 48 49
 FT SEQUENCE 303 AA; 34060 MW; 7477875BDE5F744 CRC64;
 SQ
 Query Match 21.8%; Score 270; DB 1; Length 303;
 Best Local Similarity 32.6%; Pred. No. 1.5e-14;
 Matches 71; Conservative 36; Mismatches 101; Indels 10; Gaps 4;
 QY 29 RGCEBDDALAHMFRQLFEFSTMRDPTPAQFOEHLERFOALDRSDPVSQAFVWMA 88
 DB 87 RRGTRKDGALFKFCFQNLGFVTVHNDSCAMQDLRRASBDDHNS--ACFACVLIS 143
 QY 89 HGRSEFLGDEDMKNTLPEALNNKNCQALRAKRYVITQACRGEQDPGETVGDEI 148
 DB 144 HEEELLYGKDG-VPIPIDLNAHFRGDRCKTLLEKPKLFFIOACRGTEHDDGIQANDSGPI 202
 QY 149 VWVINDSPQITPTTYDALHVVSTVEGYTAVRHDOGSGCIQTLVVFTR--RKGHILELL 206
 DB 203 NDIDANPNKPIPVADLFAVSTVPGYISWRKPGKSWFVQALCSILNEHGDLIMQTL 262
 QY 207 TQVTRMAEABIVDEGKAR---KTNPEIQSTLRRLY 240
 DB 263 TRVDNRVARRHESQSDDPFNEKQIPCMVSWLREL 300
 RESULT 11
 ID ICE7_MESAU STANDARD; PRT; 303 AA.
 AC P55214;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
 DE (ICE-LAP3) (Apoptotic protease Mch-3) (SREBP cleavage activity 2)
 DE (SCA-2).
 GN CASP7 OR MCH3.
 OS Mesocricetus auratus (Golden hamster).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RX SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RP STRAIN=Syrian; TISSUE=Liver;
 RC MEDLINE=96224303; PubMed=8643593;
 RA Pai J.-T., Brown M.S., Goldstein J.L.;
 RT "Purification and cDNA cloning of a second apoptosis-related cysteine
 protease that cleaves and activates sterol regulatory element binding
 proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).
 CC -1- FUNCTION: Involved in the activation cascade of caspases
 responsible for apoptosis execution. Cleaves and activates sterol
 regulatory element binding proteins (SREBPs). Proteolytically
 cleaves poly(ADP-ribose) polymerase (PARP) at a 216-Asp-Gly-217
 bond. Overexpression promotes programmed cell death (By
 similarity).
 CC -1- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit
 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- PTM: CLEAVAGES BY GAZZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
 SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
 CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
 VICE VERSA (By similarity).
 CC -1- SIMILARITY: Belongs to peptidase family C14.
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 or send an email to license@isb-sib.ch).

DR EMBL: U47332; AAC52595.1; -
 DR HSSP: P42574; 1PAU.
 DR MEROPS: C14.004; -
 DR InterPro: IPR002138; ICE_P10.
 DR InterPro: IPR001309; ICE_P20.
 DR InterPro: IPR002398; Peptidase C14.
 DR Pfam: PF00656; Peptidase C14; 1.
 DR PRINTS: PR00376; TLBCENZME.
 DR SMART: SM00115; CASC; 1.
 DR PROSITE: PS01122; CASPASE_C1G; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 KW Hydrolyase; thiol protease; Zymogen; Apoptosis.
 FT PROPEP 1 23
 FT CHAIN 24 198 CASPASE-7 SUBUNIT P20.
 FT PROPEP 199 206 BY SIMILARITY.
 FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.
 FT ACT_SITE 144 144 BY SIMILARITY.
 FT ACT_SITE 186 186 BY SIMILARITY.
 FT ACT_SITE 303 AA; 34037 MW; EA29356D90984648 CRC64;
 SQ SEQUENCE

Query Match 21.0%; Score 260; DB 1; Length 303;
 Best Local Similarity 31.7%; Pred. No. 9,8e-14;
 Matches 69; Conservative 39; Mismatches 100; Indels 10; Gaps 5;

OY 29 REGSEDDALHEMRQLEFSTMKRDPFAEQFOELEKFOOAIISREDPVSCAFVIMA 88
 DB 87 RKGTDADALFECFSLGFDVVVNDSCAKKQDLIRKASEDHNS--ACFACVILLS 143
 OY 89 HREGEGLKGDGEMVLENIUFEALNNKNCALRAKPKYVILQACRGEQDPGETVGDDEI 148
 DB 144 HEEENILYKGDG-VYTIKDLTAHFRRGDRCKTLEKPKLFITQCRGTELDGQVADSGPI 202
 OY 149 VWVWKDPSQTIPTPTDALTAVYSTVEGYIAVRHDQKSCFQTLVNVFTK--RKCHILELL 206
 DB 203 NEIDNAPRYKILPEADFLFAYSTVPGYVSWENDKGKSWFQALCSILDEHGKOLEITWQIL 262

OY 207 TEVTRMA---EAEVQV-E GKARKNPETQSTLRKRLY 240
 DB 263 TRVNDRAHHPESQCDPFCFNEKKQIPCMVSMILTKELY 300

RESULT 12
 ID ICE7_HUMAN STANDARD; PRT; 303 AA.
 AC P55210; Q13364; Q96BNO;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Caspase-7 precursor (BC 3.4.22.-) (ICE-like apoptotic protease 3)
 DE (ICE-LAP3) (apoptotic protease Mch-3) (CmH-1).
 GN CASP7 OR MCH3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX MEDLINE=96139498; PubMed=8576161;
 RA Duan H., Chinaiyan A.M., Hudson P.L., Wing J.P., He W.-W.,
 RA Dixit V.M.;
 RT "ICE-LAP3, a novel mammalian homologue of the Caenorhabditis elegans
 cell death protein Ced-3 is activated during Fas- and tumor necrosis
 factor-induced apoptosis.";
 RT J. Biol. Chem. 271:1621-1625 (1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RC TISSUE=Spleen;
 RX MEDLINE=96147144; PubMed=8567622;
 RA Lippe U.A., Gu Y., Sarnacki C., Caron P.R., Su M.S.-S.;
 RT "Identification and characterization of CPP32/Mch2 homolog 1, a novel
 cysteine protease similar to CPP32.";
 RT J. Biol. Chem. 271:1825-1828 (1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RC TISSUE=T-cell;
 RX MEDLINE=96105019; PubMed=8521391;
 RA Fernandez-Alnemir T., Takahashi A., Armstrong R.C., Krebs J.,
 RA Fritz L.C., Tomaselli K.J., Wang L., Yu Z., Croce C.M., Salvesson G.,
 RA Earnshaw W.C., Litwack G., Alnemir E.S.;
 RT "Mch3, a novel human apoptotic cysteine protease highly related to
 CPP32.";
 RT Cancer Res. 55:6045-6052 (1995).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND ALPHA').
 RC TISSUE=Fetal lung, and Fetal spleen;
 RX MEDLINE=97224489; PubMed=9070923;
 RA Uuan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
 RA Copeland N.G., Fletcher F.A.;
 RT "Identification and mapping of Casp7, a cysteine protease resembling
 CPP32 beta, interleukin-1 beta converting enzyme, and CED-3.";
 RT Genomics 40:86-93 (1997).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Staelestein M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Millhys S.J.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Gunaratne P.H.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,


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DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00656; Peptidase_C14; 1.
DR PRINTS: PR00376; ILBCENZYM.
DR SMART: SMO0115; CASc; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS0207; CASPASE_P10; 1.
DR PROSITE: PS0208; CASPASE_P20; 1.
KW Hydrolyse; Thiol protease; Zymogen; Apoptosis; Alternative splicing;
KW 3D-structure.
FT PROPEP      1    23
FT CHAIN       1    193
FT PROEP       1    206
FT CHAINEP     1    206
FT CHAIN       207   303
FT ACT_SITE   144   144
FT ACT_SITE   186   186
FT VASPPIC     1    1
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(in isoform Alpha').
/ftId=VSP_000806.
VITGCKGVTDIKDLTAHFRRDRCKTLLEPKLFFIOACRGT
ELDDGIQADSGPIINDTDAANRYKIPLVEADPLFAYSTVGTY
SMRSPGSGSWFOALCSILEEHKDILNIOTLRVNDRVAR
HEFSGDHPHHFKKOIPCVSMILYELKFVSQ -> MESGS
VTOAGVQRRLIGKLDPPLPAIARGSLMASREPTGPSMTQ
MLILDTRSQWKLTSSSIPRFQAIRTGAEQEAPGLCKPSA
PSMRSTEKTWKSCRSPG (in isoform Beta).
/ftId=VSP_000807.
C->A: NO APOPTOTIC ACTIVITY.
D->E (IN REF. 5)'.
G->A (IN REF. 1)'.
FT CONFLICT   4    4
FT CONFLICT   194   194
FT SOURCE     303 AA; 34276 MW; CD373BE54A232CA4 CRC64;
Query Match          20.7%; Score 256; DB 1; Length 303;
Best Local Similarity 30.7%; Pred. No. 2e-13;
Matches 67; Conservative 39; Mismatches 102; Indels 10; Gaps 4
DY REGSEEDIALAHMFROLFESETMKRDTPAQFOELEKFCQALDSREDPVSCAFVIMA 88
DB RRGDTKDXNALPKCRSLGFVDIVYNDSCKAMPDLKK--ASEEDHTNACEFACTILLS 143
QY HGRBEGFLGEDEGWVKLENLEFEALNNRNCOALARPKFYLIYAQCRGEORDGETYGEBI 148
DB HGEENVIVGGKG-VPIRIDLTAFHRGDRCKTLLEPKLFIQAQCGTFIDLDGIOADSPI 202
QY VWVIKDSQTIPTYDALHYSTVEGYIAHYHDQKSCFIQTLYDVFTK-RKHGLELL 206
DB NDTIANPYKLPVEADFLEFAYSTVPYGYSMRSPPRGSGWFVOALCSILEHDKDELMIQIL 262
QY TEVTNRMAEAELVDEG---KARKYLEIESTLKRLRY 240
DB TVANDRVARRHPSQSDDPHHEKKGQICVVSMILTLEY 300

RESULT 13
ID _CASEL STANDARD; PRT; 503 AA.
AC P45753; P45435; Q9G0Q4; Q9NAO8;
DT 01-NOV-1995 (Rel. 32, Created);
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cell death protein 3 precursor (EC 3.4.22.-).
GN CED-3 OR C4BD1.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Rhabditoidea;
OC Rhabditiidae; Paludorinae; Caenorbabitids.
OX NCBI_TaxId=6239;
EN [ ]
RP SEQUENCE FROM N.A., AND MUTAGENESIS.
RC STRAIN=Bristol N2;.
RX MEDLINE=94061982; PubMed=8242740;
YU Yuan J.; Shaham S.; Ledoux S. Filling u

```


RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
RA Jatali M., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laake P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mount S.N., Moy M., Murphy B., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nussken D.R., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spieding A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkeley; TISSUE=Head;
RC MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Garin H., Krommiller B., Pacleib J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.E.;
RT "A Drosophila full-length cDNA resource";
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Acts downstream of rpr.
CC Cleaves baculovirus p35 and lamin Dmo in vitro.
CC -1- SUBUNIT: Heterodimer of a 21 kDa (p21) and a 12 kDa (p12) subunit.
CC -1- DEVELOPMENTAL STAGE: Expressed at all stages where apoptosis
CC occurs.
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL: Y1261; CAA72937.1; -
CC EMBL: AE003771; AAF5639.1; -
CC EMBL: AY058451; AML13680.1; -
CC HSP, P42574; 1PNU.
CC
CC MEROPS: C14.015; -
CC DR FLYbase; FBgn0019972; Ice.
CC DR GO; GO:0004207; P:effector caspase activity; NAB.
CC DR GO; GO:0006915; P:apoptosis; NAB.
CC DR InterPro; IPR002138; ICE p10.
CC DR InterPro; IPR002139; ICE p20.
CC DR InterPro; IPR002398; Peptidase C14.
CC DR Pfam; PF00656; Peptidase C14; 1.
CC DR PRINTS; PR00376; IL1BCENZYM.
CC DR SMART; SM00115; CASc; 1.
CC DR PROSITE; PS01122; CASPASE_CYS; 1.
CC DR PROSITE; PS01121; CASPASE_HIS; 1.
CC DR PROSITE; PS0207; CASPASE_P10; 1.
CC DR PROSITE; PS0208; CASPASE_P20; 1.
CC DR Hydroxylase; Thiol protease; Zymogen; Apoptosis.
CC FT PROPEP 1 28 BY SIMILARITY.
CC FT CHAIN 29 217 CASPASE SUBUNIT P21 (BY SIMILARITY).
CC FT PROPEP 218 230 BY SIMILARITY.
CC FT CHAIN 231 339 CASPASE SUBUNIT P12 (BY SIMILARITY).
CC FT ACT_SITE 169 169 BY SIMILARITY.
CC FT ACT_SITE 211 211 BY SIMILARITY.
CC FT CONFLICT 151 151 A -> S (IN REF. 1).
CC FT CONFLICT 265 265 S -> T (IN REF. 1).
CC SEQUENCE 339 AA; 37363 MW; E105BD29518507EC CRC64;

Query Match 20.0%, Score 247.5; DB 1; Length 339;
Beet local similarity 30.5%; Pred. No. 1,1e-12;
Matches 60; Conservative 42; Mismatches 76; Indels 19; Gaps 5;
Qy 27 KARGSEDDALAHMROQLRFBSTMKRDPFAEPQOELEKFGQAIDSRDPVSCAFVYL 86
Db 110 KSRGVTVDENLIRLVKQDFEYTVKDC---RYKILRTIEVAASQNHSDSCILVAI 166
Qy 87 MAHGREFFLKGDEDEMYKLENTFEALNNKQALRAKPKYVITQACGEQDPBETV--- 143
Db 167 LSHHEMYIYIAKQY KLDNIMSFYANRCPISLAKRKFITQACQGRDLDGVTWQRS 225
Qy 144 ---GGDEIYVWIKSDPQITPTDYLHVYSTVEGYIAYRHDKSCFCITLVVFTK-- 197
Db 226 QETEDG-----SSMYKIPVHADFLIAYSTVGFYSWNTTSGSNFMQSLCAFLANG 279
Qy 198 RKCHITELLTEVTRMA 214
Db 280 KRDLITLTFVCQRYA 296
RESULT 15
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AC Q14750; Q14676; Q14791; Q14792; Q14793; Q14794; Q14795; Q14796;
AC Q15780; Q15806; Q8TD11; Q8TD12; Q8TD13; Q8TD14; Q8TD15; Q96T22;
AC Q9C084; Q9U081;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caspase-8 precursor (BC 3.4.22.-) (ICE-like apoptotic protease 5)
DE (MORT1-associated CED-3 homolog) (MACH) (FADD-homologous ICE/CED-3-
DE like protease) (FADD-like ICE) (FLICE) (Apoptotic cysteine protease)
DE (Apoptotic protease Mch-5) (CASP4).
GN CASP8 OR MCH5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 5; 6; 7 AND 8).
RX TISSUE=B-cell, and thymus;
RC MEDLINE=96279626; PubMed=8681376;
RA Boldin M.P., Goncharov T.M., Golitssev Y.V., Wallach D.;
RT "Involvement of MACH, a novel MORT1/FADD-interacting protease, in
RT Fas/Apo-1- and TNF receptor-induced cell death.";
RL Cell 85:803-815(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
RX MEDLINE=96279627; PubMed=8681377;
RA Muzio M., Chinaiyan A.M., Kischkel F.C., O'Rourke K., Shevchenko A.,
RA Ni J., Scaffidi C., Bretz J.D., Zhang M., Gentz R., Mann M.,
RA Krammer P.H., Peter M.E., Dixit V.M.;
RT "FLICE, a novel FADD-homologous ICE/CED-3-like protease, is recruited
RT to the CD95 (Fas/Apo-1) death-inducing signaling complex.";
RL Cell 85:817-827(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RC TISSUE=T-cell;
RX MEDLINE=96353838; PubMed=8755496;
RA Fernandez-Alnemri T., Armstrong R.C., Krebe J.F., Srinivasula S.M.,
RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
RA Litwack G., Alnemri E.S.;
RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RT apoptotic cysteine protease containing two FADD-like domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=99132295; PubMed=9931493;
RA Grenet J., Teitz T., Wei T., Valentine V., Kidd V.J.;
RT "Structure and chromosome localization of the human CASP8 gene.";
RL Gene 226:225-232(1999).

[5]
SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=97375543; PubMed=9228018;
RA Srinivasula S.M., Ahmad M., Oltjelle S., Bullrich F., Banks S.,
RA Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,
RA Armstrong R.C., Alnemri E.S.,
RA "FAME-1, a novel FADD-like anti-apoptotic molecule that regulates
RT Fas/TNFR1-induced apoptosis.";
RT J. Biol. Chem. 272:18542-18545 (1997).
RL [6]
SEQUENCE FROM N.A.
MEDLINE=21100893; PubMed=1161814;
RA Hadano S., Yamagisawa Y., Skaug U., Fichter K., Nasir J.,
RA Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
RA Ikeda J.-E., Hayden M.R.,
RT "Cloning and characterization of three novel genes, A152CR1, A152CR2,
RT and A152CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
RT critical region at chromosome 2q33-q34: candidate genes for ALS2.";
RL Genomics 71:200-213 (2001).
RN [7]
SEQUENCE FROM N.A. (ISOFORM 7), AND FUNCTION OF ISOFORM 7.
RC TISSUE=Leukocyte;
MEDLINE=22005982; PubMed=12010809;
RA Himeji D., Horituchi T., Tsukamoto H., Hayashi K., Watanabe T.,
RA Harada M.,
RT "Characterization of caspase-8L: a novel isoform of caspase-8 that
RT behaves as an inhibitor of the caspase cascade.";
RL Blood 99:4070-4078 (2002).
RN [8]
SEQUENCE FROM N.A. (ISOFORMS 1, 2 AND 9), AND INTERACTION OF ISOFORM 9
RP WITH BCAP31 AT THE ENDOPLASMIC RETICULUM.
MEDLINE=21927603; PubMed=11917123;
RA Breckenridge D.G., Nguyen M., Kupzig S., Reith W., Shore G.C.,
RT "The procaspase-8 isoform, procaspase-8L, recruited to the BAP31
RT complex at the endoplasmic reticulum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4331-4336 (2002).
RN [9]
SEQUENCE FROM N.A. (ISOFORM 7).
RC TISSUE=Leukocyte;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Millar J.S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Wiley J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [10]
PARTIAL SEQUENCE, AND PROCESSING.
MEDLINE=97121412; PubMed=8962078;
RA Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
RA Alnemri E.S.,
RT "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1
RT protease Mcm5 is a CrmA-inhibitable protease that activates multiple
RT Ced-3/ICE-1-like cysteine proteases.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491 (1996).
RN [11]
FUNCTION.
MEDLINE=97160607; PubMed=9006941;
RA Muzio M., Salvesen G.S., Dixit V.M.,
RT "FICE induced apoptosis in a cell-free system. Cleavage of caspase
RT zymogens.";
RL J. Biol. Chem. 272:2952-2956 (1997).
RN [12]
PROCESSING.
MEDLINE=97327557; PubMed=9184224;
RA Medema J.P., Scalfidi C., Kischkel F.C., Shevchenko A., Mann M.,
RA Kramer P.H., Peter M.B.,
RT "FICE is activated by association with the CD95 death-inducing
RT signaling complex (DISC)."
RL EMBO J. 16:2794-2804 (1997).
RN [13]
CHARACTERIZATION OF ISOFORM 7.
MEDLINE=20318377; PubMed=10860845;
RA Horituchi T., Himeji D., Tsukamoto H., Harashima S., Hashimura C.,
RA Hayaishi K.,
RT "Dominant expression of a novel splice variant of caspase-8 in human
RT peripheral blood lymphocytes.";
RL Biochem. Biophys. Res. Commun. 272:877-881 (2000).
RN [14]
INTERACTION WITH BCL2, BCL2L1 AND BCAP31.
MEDLINE=97477382; PubMed=934338;
RA Ng F.W.H., Nguyen M., Kwan T., Branton P.E., Nicholson D.W.,
RA Cromlish J.A., Shore G.C.,
RT "p28 Bap31, a Bcl-2/Bcl-XL- and procaspase-8-associated protein in the
RT endoplasmic reticulum.";
RL J. Cell Biol. 139:327-338 (1997).
RN [15]
INTERACTION WITH PEAL5.
MEDLINE=99369240; PubMed=10442631;
RA Condorelli G., Vigiotti G., Cafieri A., Trencia A., Andalo P.,
RA Oriente F., Mele C., Caruso M., Fornisano P., Beggiato F.,
RT "PEP/PEA-15: an anti-apoptotic molecule that regulates Fas/TNFR1-
RT induced apoptosis.";
RL Oncogene 18:4409-4415 (1999).
RN [16]
X-RAY CRYSTALLOGRAPHY (2.8 ÅGSTROMS).
MEDLINE=99451259; PubMed=10508784;
RA Blanchard H., Kodandapani L., Mittl P.R.E., Di Marco S., Krebs J.F.,
RA Wu J.C., Tomaselli K.J., Gnetter M.G.,
RT "The three-dimensional structure of caspase-8: an initiator enzyme in
RT apoptosis.";
RL Structure 7:1125-1133 (1999).
RN [17]
VARIANT CASP8D TRP-248.
MEDLINE=2239940; PubMed=12353035;
RA Chun H.J., Zheng L., Ahmad M., Wang J., Speirs C.K., Siegel R.M.,
RA Dale J.K., Puck J., Davis J., Hall C.G., Skoda-Smith S.,
RA Atkinson T.P., Straus S.E., Ienardo M.J.,
RT "pleiotropic defects in lymphocyte activation caused by caspase-8
RT mutations lead to human immunodeficiency.";
RL Nature 419:395-399 (2002).
RN -1- FUNCTION: Most upstream protease of the activation cascade of
CC caspases responsible for the TNFRSF6/Fas mediated and TNFRSF1A
CC induced cell death. Binding to the adapter molecule FADD recruits
CC it to either receptor. The resulting aggregate called death-
CC inducing signaling complex (DISC) performs CASP8 proteolytic
CC activation. The active dimeric enzyme is then liberated from the
CC DISC and free to activate downstream apoptotic proteases.
CC Proteolytic fragments of the N-terminal propeptide (termed CAP3,
CC CAP5 and CAP6) are likely retained in the DISC. Cleaves and
CC activates CASP3, CASP4, CASP6, CASP7, CASP9 and CASP10. May
CC participate in the G2M6 apoptotic pathways. Cleaves ADPRT.
CC Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-I-AMC.
CC likely target for the cowpox virus CRMA death inhibitory protein.
CC Isoforms 5, 6, 7 and 8 lack the catalytic site and may interfere
CC with the pro-apoptotic activity of the complex.
CC -1- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 10 kDa (p10) subunit.
CC Interacts with FADD, CFLAR and PEAL5. Isoform 9 interacts at the
CC endoplasmic reticulum with a complex containing BCAP31, BAP29,
CC BCL2 and/or BCL2L1.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS:

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CC Event-Alternative splicing; Named isoforms=9;
CC Name=1; Synonyms=Alpha-1;
CC IsoId=Q14790-1; Sequence=Displayed;
CC Name=2; Synonyms=Alpha-2, MCH5-beta;
CC IsoId=Q14790-2; Sequence=VSP_000610;
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Run on: July 12, 2004, 13:45:17 ; Search time 21 seconds
(without alignments)
594.928 Million cell updates/sec

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Sequence:

Scoring table: BLOSUM62
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Searched: 369414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 369414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	1239	100.0	242	4	US-09-187-789-5 Sequence 5, Appli
2	1065	86.0	214	4	US-09-187-789-9 Sequence 9, Appli
3	934.5	75.4	260	4	US-09-187-789-2 Sequence 2, Appli
4	934.5	75.4	260	4	US-09-139-600-2 Sequence 2, Appli
5	890	71.8	230	4	US-09-187-789-7 Sequence 7, Appli
6	293	23.6	74	4	US-09-187-789-63 Sequence 58, Appli
7	293	23.6	74	4	US-09-139-600-58 Sequence 10, Appli
8	289	23.3	421	4	US-08-983-502-10 Sequence 10, Appli
9	289	23.3	421	4	US-09-516-747-10 Sequence 10, Appli
10	289	23.3	421	5	PCT-US96-10521-10 Sequence 10, Appli
11	289	23.3	435	3	US-08-258-287B-53 Sequence 51, Appli
12	289	23.3	435	3	US-08-368-704C-51 Sequence 9, Appli
13	289	23.3	435	3	US-09-561-756-9 Sequence 9, Appli
14	289	23.3	435	4	US-09-227-721-9 Sequence 2, Appli
15	289	23.3	435	4	US-08-816-075-2 Sequence 9, Appli
16	289	23.3	435	4	US-08-724-378D-9 Sequence 9, Appli
17	289	23.3	435	4	US-09-954-697-9 Sequence 4, Appli
18	289	23.3	435	5	PCT-US94-07127A-4 Sequence 44, Appli
19	289	23.3	441	3	US-08-258-287B-44 Sequence 43, Appli
20	289	23.3	441	3	US-08-368-704C-43 Sequence 10, Appli
21	279	22.5	435	4	US-09-291-289-10 Sequence 2, Appli
22	278.5	22.1	277	2	US-08-890-542A-2 Sequence 2, Appli
23	278.5	22.1	277	3	US-08-591-605-2 Sequence 2, Appli
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27	273.5	22.1	277	4	US-09-069-138-6 Sequence 6, Appli

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39	263.5	21.3	277	3	US-08-964-313-10 Sequence 10, Appli
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42	257	20.7	503	3	US-08-368-704C-36 Sequence 24, Appli
43	256	20.7	303	4	US-09-561-756-24 Sequence 24, Appli
44	256	20.7	303	4	US-09-227-721-24 Sequence 24, Appli
45	256	20.7	303	4	US-08-556-627A-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-187-789-5
; Sequence 5, Application US/09187789
; Patent No. 6340740

GENERAL INFORMATION:
; APPLICANT: Alnemir, Emaad S.
; APPLICANT: Fernandez-Alnemir, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C1
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-187-789-5

Query Match 100.0%; Score 1239; DB 4; Length 242;
Best Local Similarity 100.0%; Pred. 0.3-2e-122;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	61	FOELEKFGQALISREDPVSCAFVVMMAHREBFTKSGDEGMYKLELFEALNNKNCAL	120
QY	121	RARKXYITLACGEORDPETVSGDEIYVWIKDSFOTIPTYTDALHVSIVGCIAYRH	180
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RESULT 2
US-09-187-789-9
; Sequence 9, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:

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; APPLICANT: Alnemri, Emed S.
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-187-789-9
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Best Local Similarity 88.0%; Pred. No. 5.3e-104;
Matches 213; Conservative 0; Mismatches 1; Indels 28; Gaps 1;
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QY 1 MSNRSLEEEKYDMSGALALILCVTKAREGSEEDLDALBHMFRQLRFESTMKRDPYAEQ 60
D 1 MSNRSLEEEKYDMSGARLALILCVTKAREGSE-----34
QY 61 FOELEKFOQAIDSRDPVSCAFVYVMAHGREGLKSGDEGMVLENI,FEALNNKNCQAL 120
D 35 --BELEKFOQAIDSRDPVSCAFVYVMAHGREGLKSGDEGMVLENI,FEALNNKNCQAL 92
QY 121 RAKPKVYIIQACRGQRDPGSETVGDEIVWYIKDSPOTIPYTDALHVSIVSGYIAYRH 180
D 93 RAKPKVYIIQACRGQRDPGSETVGDEIVWYIKDSPOTIPYTDALHVSIVSGYIAYRH 152
QY 181 DQKSGCTIQLTVDFVTFKRKHIIELTEVTRMAAEI,VOEGARKATNPEIQSTLRKELY 240
D 153 DQKSGCTIQLTVDFVTFKRKHIIELTEVTRMAAEI,VOEGARKATNPEIQSTLRKELY 212
QY 241 LQ 242
D 213 LQ 214
```

```

RESULT 3
US-09-187-789-2
; Sequence 2, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emed S.
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-2
```

```

Query Match      75.4%; Score 934.5; DB 4; Length 260;
Best Local Similarity 70.9%; Pred. No. 3.6e-90;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;
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```

QY 1 MSNRSLEEEKYDMSGALALILCVTKAREGSEEDLDALBHMFRQLRFESTMKRDPYAEQ 60
D 8 MSDDPQLQBERYDMSGARLALILCVTKAREGSEVDMEALERMFRYLFKESTMKRDPYAEQ 67
QY 61 FOELEKFOQAIDSRDPVSCAFVYVMAHGREGLKSGDEGMVLENI,FEALNNKNCQAL 120
D 68 FLEELDEFOQTIDMEBPVSCAFVYVMAHGREGLKSGDEGMVLENI,FEALNNKNCQAL 127
QY 121 RAKPKVYIIQACRGQRDPG-----ETVGGDEIVWYIKDSPOTIPYTDALHVS 168
```

```

D 128 RKKPKVYIIQACRGHRDPGEEELRGNEELGDEBELGDE-VAVLKNNGQSIPTTYDTLHI 186
QY 169 YSTVGYIAYRHDDQSGCFIQLTVDFVTFKRKHIIELTEVTRMAAEI,VOEGARKATN 228
D 187 YSTVGYIAYRHDDQSGCFIQLTVDFVTFKRKHIIELTEVTRMAAEI,VOEGARKATN 246
QY 229 PEIQSTLRKRLYIQ 242
D 247 PEVQSTLRKRLYIQ 260
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```

RESULT 4
US-09-139-600-2
; Sequence 2, Application US/09139600
; Patent No. 6432628
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emed S.
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434
; CURRENT APPLICATION NUMBER: US/09/139,600
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-2
```

```

Query Match      75.4%; Score 934.5; DB 4; Length 260;
Best Local Similarity 70.9%; Pred. No. 3.6e-90;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;
```

```

QY 1 MSNRSLEEEKYDMSGALALILCVTKAREGSEEDLDALBHMFRQLRFESTMKRDPYAEQ 60
D 8 MSDDPQLQBERYDMSGARLALILCVTKAREGSEVDMEALERMFRYLFKESTMKRDPYAEQ 67
QY 61 FOELEKFOQAIDSRDPVSCAFVYVMAHGREGLKSGDEGMVLENI,FEALNNKNCQAL 120
D 68 FLEELDEFOQTIDMEBPVSCAFVYVMAHGREGLKSGDEGMVLENI,FEALNNKNCQAL 127
QY 121 RAKPKVYIIQACRGQRDPG-----ETVGGDEIVWYIKDSPOTIPYTDALHVS 168
D 128 RKKPKVYIIQACRGHRDPGEEELRGNEELGDEBELGDE-VAVLKNNGQSIPTTYDTLHI 186
QY 169 YSTVGYIAYRHDDQSGCFIQLTVDFVTFKRKHIIELTEVTRMAAEI,VOEGARKATN 228
D 187 YSTVGYIAYRHDDQSGCFIQLTVDFVTFKRKHIIELTEVTRMAAEI,VOEGARKATN 246
QY 229 PEIQSTLRKRLYIQ 242
D 247 PEVQSTLRKRLYIQ 260
```

```

RESULT 5
US-09-187-789-7
; Sequence 7, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emed S.
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 230
```


TYPE: PRT
ORGANISM: Homo sapien
US-09-187-789-7

Query Match 71.8%; Score 890; DB 4; Length 230;
Best Local Similarity 99.4%; Pred. No. 1.5e-85;
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNRSRLSEEEKYDMSGALALILCVTKAREGSEEDLDLHEMPROLPESTMKRDPFAEQ 60
DB 1 MSNRSRLSEEEKYDMSGALALILCVTKAREGSEEDLDLHEMPROLPESTMKRDPFAEQ 60
QY 61 FOEIELEKFOQAIDSRDEPVSCAFVILMAHREGFLKGDGEWVKLENLFEALNNKCOAL 120
DB 61 FOEIELEKFOQAIDSRDEPVSCAFVILMAHREGFLKGDGEWVKLENLFEALNNKCOAL 120
QY 121 RAKPKVYIIQACRGQRDPGETVGDVIMVTKDSPQITPTTALHYSTVEG 174
DB 121 RAKPKVYIIQACRGQRDPGETVGDVIMVTKDSPQITPTTALHYSTVEG 174

RESULT 6
US-09-187-789-63

Sequence 63, Application US/09187789

Patent No. 6340740

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

APPLICANT: Fernandez-Alnemri, Teresa

TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING

TITLE OF INVENTION: AND METHODS OF USE

FILE REFERENCE: 480140.434C1

CURRENT APPLICATION NUMBER: US/09/187,789

CURRENT FILING DATE: 1998-11-06

NUMBER OF SEQ ID NOS: 78

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 63

LENGTH: 74

TYPE: PRT

ORGANISM: Mus musculus

US-09-187-789-63

Query Match 23.6%; Score 293; DB 4; Length 74;
Best Local Similarity 77.8%; Pred. No. 1.6e-23;
Matches 56; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 28 ARGSEEDLDLHEMPROLPESTMKRDPFAEQFOEIELEKFOQAIDSRDEPVSCAFVILM 87
DB 1 ARGSEEDLDLHEMPROLPESTMKRDPFAEQFOEIELEKFOQAIDSRDEPVSCAFVILM 87

QY 88 AHREGFLKGED 99
DB 61 AHREGFLKGED 72

RESULT 7
US-09-139-600-58

Sequence 58, Application US/09139600

Patent No. 6432628

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

APPLICANT: Fernandez-Alnemri, Teresa

TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING

TITLE OF INVENTION: AND METHOD OF USE

FILE REFERENCE: 480140.434

CURRENT APPLICATION NUMBER: US/09/139,600

CURRENT FILING DATE: 1998-08-25

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 58

LENGTH: 74

TYPE: PRT

ORGANISM: Mus musculus

US-09-139-600-58

Query Match 23.6%; Score 293; DB 4; Length 74;
Best Local Similarity 77.8%; Pred. No. 1.6e-23;
Matches 56; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 28 ARGSEEDLDLHEMPROLPESTMKRDPFAEQFOEIELEKFOQAIDSRDEPVSCAFVILM 87
DB 1 ARGSEEDLDLHEMPROLPESTMKRDPFAEQFOEIELEKFOQAIDSRDEPVSCAFVILM 87

QY 88 AHREGFLKGED 99
DB 61 AHREGFLKGED 72

RESULT 8
US-08-983-502-10

Sequence 10, Application US/08983502

Patent No. 6399327

GENERAL INFORMATION:

APPLICANT: David WALLACH

APPLICANT: Mark P. BOLDIN

APPLICANT: Tanya M. GONCHAROV

TITLE OF INVENTION: YUZY V. GOLTSSEV

TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSER: Broadway and Neimark

STREET: 419 Seventh Street N.W., Ste. 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/983,502

FILING DATE: 16-JAN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/10521

FILING DATE: 14-JUN-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 114,615

FILING DATE: 16-JUL-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 114,986

FILING DATE: 17-AUG-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 115,319

FILING DATE: 14-SEP-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 116,588

FILING DATE: 27-DEC-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 117,932

FILING DATE: 16-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Broadway, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: WALLACH-19

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-5197

TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 421 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-983-502-10

Query Match 23.3%; Score 289; DB 4; Length 421;
Best Local Similarity 31.1%; Pred. No. 5,2e-22;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

29 REGSEDDDALEHMRQRFESTMKRDPFAEQFOELEKFOQALDSREDPVSACAFVIMA 88
188 RSGGVDSHTVLTFLKLGVDVHVLCDQTAQEMQEKLNFAQ-LPAHRTVDSCLVALLS 245
89 HGRGFLKGEDEWYKLENTLEALNNKNCQALRAKPKYIIIOACGEGRDG----- 140
246 HGVEGATVGVGSKLLQAEVQLFDNANCPSLQNKPKYFIQACRGDETDGVDQODGKN 305
141 -----ETVGGDEIVWIKDSPQITPTDALTAVYSTVEGYIAYRHQDQSCFIQTLV 192
306 HAGSPGCEESDAGE-----KLPRKRLPTRSDMI CGVACLGSTAMNTKRGSWITEALA 360
QY 193 DVFTKR--KGHILELLEVTNRMAAEALVQEGKARKTN-----PEIQTIRRLRYL 241
Db 361 QVFSERACDVHADVADMLVKYNALIKD---REGVAPGTEFHRCKEMSEYCSITLCRHLYL 414

RESULT 9

US-09-516-747-10
Sequence 10, Application US/09516747
Patent No. 6586571

GENERAL INFORMATION:

APPLICANT: David WALLACH
Mark P. BOLDIN
Tanya M. GONCHAROV

TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
AND OTHER PROTEINS

NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:

ADDRESSEE: Broadway and Neimark
STREET, 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,747
FILING DATE: 01-Mar-2000

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/983,502
FILING DATE: <Unknown>
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995

APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995

APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996

ATTORNEY/AGENT INFORMATION:
NAME: Broadway, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-19

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-516-747-10

Query Match 23.3%; Score 289; DB 4; Length 421;
Best Local Similarity 31.1%; Pred. No. 5,2e-22;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

29 REGSEDDDALEHMRQRFESTMKRDPFAEQFOELEKFOQALDSREDPVSACAFVIMA 88
188 RSGGVDSHTVLTFLKLGVDVHVLCDQTAQEMQEKLNFAQ-LPAHRTVDSCLVALLS 245
89 HGRGFLKGEDEWYKLENTLEALNNKNCQALRAKPKYIIIOACGEGRDG----- 140
246 HGVEGATVGVGSKLLQAEVQLFDNANCPSLQNKPKYFIQACRGDETDGVDQODGKN 305
141 -----ETVGGDEIVWIKDSPQITPTDALTAVYSTVEGYIAYRHQDQSCFIQTLV 192
306 HAGSPGCEESDAGE-----KLPRKRLPTRSDMI CGVACLGSTAMNTKRGSWITEALA 360
QY 193 DVFTKR--KGHILELLEVTNRMAAEALVQEGKARKTN-----PEIQTIRRLRYL 241
Db 361 QVFSERACDVHADVADMLVKYNALIKD---REGVAPGTEFHRCKEMSEYCSITLCRHLYL 414

RESULT 10

PCT-US96-10521-10
Sequence 10, Application PC/TUS9610521

GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
AND OTHER PROTEINS

NUMBER OF SEQUENCES: 34
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10521-10

Query Match 23.3%; Score 289; DB 5; Length 421;
Best Local Similarity 31.1%; Pred. No. 5,2e-22;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

QY 29 EGGSEBDLALHEMRQALRFESTMKRDPRAEFOEIEKFOOALBSREDPVSCAFVLMA 88
 Db 188 RSGGVNDSTLTVLTKFLGVDVHVLCDOTJAEQKQLQVFAQ-LPRHRTDSC-YALLS 245
 QY 89 HGRGEFLGEGDEQEWKLENTFEALNNKNCQALRAKPKVYIIQAQSGQRDPG----- 140
 Db 246 HGVEBAITGVDPDKTLQLEQVFOLEFNPANCSLQNKPKMFFIQACRDEDTEDRGVDOODGXN 305
 QY 141 -----ETVGGDEIVMTIKDSPOILPIFYTALNHYSVEGIIAYRHQKSGCFIQTV 192
 Db 306 HAGSDGCEESDQKGE-----KLPRKRLPIRSDITCGAALCKGTAAENNTYKGSWYIEALA 360
 QY 193 DVETPR--KGIHLELLEVTTRMAAEALVQEGAKRTN-----PEIQSTLKRRLYL 241
 Db 361 QVFSERACMAYADMLVKYNALLKD---REGVAPQTEPHRCKEMSPYSTLCRHLYL 414

```

1      RESULT 11
2      US-08-258-287B-53
3      / Sequence 53, Application US/08258287B
4      / Patent No. 6083735
5      / GENERAL INFORMATION:
6      / APPLICANT: Yuan, Junying
7      / APPLICANT: Mura, Masayuki
8      / TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
9      / NUMBER OF SEQUENCES: 85
10     / CORRESPONDENCE ADDRESS:
11     / ADDRESSEE: Sterne, Kessler, Goldstein & Fox
12     / STREET: 1100 New York Avenue, Suite 600
13     / CITY: Washington
14     / STATE: D.C.
15     / COUNTRY: USA
16     / ZIP: 20005
17     / COMPUTER READABLE FORM:
18     / MEDIUM TYPE: Floppy disk
19     / COMPUTER: IBM PC compatible
20     / OPERATING SYSTEM: PC-DOS/MS-DOS
21     / SOFTWARE: PatentIn Release #1.0, Version #1.25
22     / CURRENT APPLICATION DATA:
23     / APPLICATION NUMBER: US/08/258,287B
24     / FILING DATE: 10-JUN-1994
25     / CLASSIFICATION: 435
26     / PRIOR APPLICATION DATA:
27     / APPLICATION NUMBER: US 08/080,850
28     / FILING DATE: 24-JUN-1993
29     / ATTORNEY/AGENT INFORMATION:
30     / NAME: Bugalsky, Lawrence B.
31     / REGISTRATION NUMBER: 35,086
32     / REFERENCE/DOCKET NUMBER: 0609.3920001
33     / TELECOMMUNICATION INFORMATION:
34     / TELEPHONE: (1202) 371-2600
35     / TELEFAX: (202) 371-2540
36     / TELEX: 248636 SSK
37     / INFORMATION FOR SEQ ID NO: 53:
38     / SEQUENCE CHARACTERISTICS:
39     / LENGTH: 435 amino acids
40     / TYPE: amino acid
41     / TOPOLOGY: linear
42     / MOLECULE TYPE: protein
43     /
44     / US-08-258-287B-53

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Query Match	23.3%;	Score 289;	DB 3;	Length 435;
Best Local Similarity	31.1%;	Pred. No. 5.4e-22;		
Matches 74;	Conservative 51;	Mismatches 77;	Indels 36;	Gaps 7;

QY 29 REGSSESDIDALEHMRFOLEFESTMKDPAEFOEELERFOALDSREBVSQAEVILIA 38
Db 202 RSGGVDSHTVTLERKLGVDVHVLCDQJAEQEXLQNAQ_LPHARVTDSC-IALLS 259
QY 89 HGRSGFLKGEDEMWKLEMLFEALNNKNNQALRAKRYVTLQACRSGQDPG----- 140
Db 260 HGVEFAIIVGDSKLLQLOEVEFQLEPDANCELSLNKKKMFLLQCRSGEDTRGVQDDGKN 319

```

QY -----ETVGGDEIVWIKSPQITPIYTDALHYSVEEGIAVRHOKSGCEIOTIV 192
141 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db HAGSPGCEESDQKE-----KLPKXRLPFRSDMICYALCKGTAAARNTRRGSGMYIEALA 374
QY -----DVETFR--KCHITLLEITVETFRMAEELVVOEGARKTN-----PEIOSTLKRRL 241
193 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db QVFSRACDMVADMLVKNALIKD-----REGVAPGTEHFRCKEMSEYCTTLCRHLYL 428

```

```

RESULT 12
US-08-368-704C-51
/ Sequence 51, Application US/08368704C
/ Patent No. 6087160
/ GENERAL INFORMATION:
/ APPLICANT: Yuan, Junying
/ APPLICANT: Mitura, Masayuki
/ TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
/ NUMBER OF SEQUENCES: 95
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sterne, Kessler, Goldstein & Fox
/ STREET: 1100 New York Avenue, Suite 600
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/368,704C
/ FILING DATE: 4-JAN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/259,287
/ FILING DATE: 10-JUN-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/080,850
/ FILING DATE: 24-JUN-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bugalsky, Lawrence B.
/ REGISTRATION NUMBER: 35,086
/ REFERENCE/DOCKET NUMBER: 0609.3920002
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 371-2600
/ TELEFAX: (202) 371-2540
/ TELEX: 248636 SSK
/ INFORMATION FOR SEQ ID NO: 51:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 435 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
US-08-368-704C-51

```

Query Match	23.3%;	Score 289;	DB 3;	Length 435;
Best Local Similarity	31.1%;	Pred. No. 5.4e-22;		
Matches 74;	Conservative 51;	Mismatches 77;	Indels 36;	Gaps 7

```

QY      29  LEGSEDEDLALHEHMRQALRFESTMKRDLPAEFOFSELEFQOALISREBPVSCAFVLWA  88
Db      202  RSGGVNDSTLVTLEFKLGYDVNVLCDOTQAOEMQELQNFAO-LPHNRVYDSC-IYALLS  259

QY      89  HGREGFLKGEDEMWKLENTLEFALNNKNCOALRAKPKVYLIQACRGEORDPG-----  140
Db      260  HEVEGALIVGVDKLLQLQLEVPFLFNANCPRSIQNKPKMFFIQACRDEDETRGVDDQDGN  319

QY      141  -----ETVAGDEIVWIKDSPOTIPTTDLAHYSTVEGYIAYRHQKSGSCFIQTLV  192
Db      320  HAGSPGCEBSDMGKE-----KLPHKRIIPRSMITGVACLKGTANRNTTGGSWYTEALA  374

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QY 193 DVFTKR--KGHLELITEVTRMAEELVVOEGKARKTN-----PEIOSTLRRLYYL 241
Db 375 QVESERACDMHVDMLVKVNNALIKD---RGGYAPGTEFHRCCKEMSEYCSSTLCRHLYYL 428

Search completed: July 12, 2004, 13:51:57
Job time : 22 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 12, 2004, 13:44:06 ; Search time 17.5 Seconds
(without alignments)
1330.191 Million cell updates/sec

Title: US-10-068-564-5

Perfect score: 1239

Sequence: 1 MSNPRSLBEKKYMSGALAL.....KARKTNPEIGSTLRRLRLYLQ 242

Scoring table: BLOSUM62

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1234	99.6	242	2 JC7517	caspase-14/a - hum
2	293	93.6	452	2 JC6507	caspase-2 - rat
3	289	23.3	435	2 A54821	apoptosis regulato
4	282.5	22.8	277	2 JC5410	CPB3 protein - mo
5	280.5	22.6	277	2 S64710	cysteine proteinas
6	272.5	22.0	277	2 A55315	cysteine proteinas
7	264.5	21.3	454	2 JC7123	caspase-9 long cha
8	248.5	20.1	503	2 A49429	interleukin-1 beta
9	246.5	19.9	212	2 I67437	cysteine proteinas
10	239.5	19.3	416	2 G02655	ICB-LAP6 human
11	230	18.6	495	2 T20038	hypothetical prote
12	226	18.2	311	2 B56084	interleukin-1beta
13	226	18.2	383	2 A56084	interleukin-1beta
14	226	18.2	404	2 A42677	interleukin-1 beta
15	225	18.2	418	2 B57511	interleukin-1 beta
16	217.5	17.6	402	2 A46495	IL-1 beta converta
17	213.5	17.2	182	2 I67436	interleukin-1-beta
18	210.5	17.0	826	2 T43638	caspase-related pr
19	207	16.7	263	2 C56084	interleukin-1beta
20	205.5	16.6	377	2 A57511	interleukin-1 beta
21	197	15.9	312	2 B54821	apoptosis regulato
22	189	15.3	536	2 T43633	caspase-related pr
23	185	14.9	488	2 T13385	hypothetical prote
24	174.5	14.1	642	2 T27021	hypothetical prote
25	159.5	12.9	136	2 I53300	interleukin-1-beta
26	103.5	8.4	1313	2 A48467	myosin heavy chain
27	98	7.9	1957	2 A45627	myosin heavy chain
28	97.5	7.8	139	2 T43642	caspase protein 3
29	97	7.8	1051	2 T18302	apb protein - Eme

30	95.5	7.7	1190	2 E84193
31	95.5	7.7	2104	2 T38774
32	95	7.7	761	2 B22205
33	91	7.3	394	2 T26968
34	91	7.3	510	2 S42626
35	90.5	7.3	520	2 F70350
36	89.5	7.2	467	2 D95253
37	89.5	7.2	482	2 B98118
38	89.5	7.2	1225	2 A56514
39	89	7.2	352	2 T43328
40	88.5	7.1	149	2 T43637
41	88.5	7.1	661	2 B97733
42	88.5	7.1	858	1 IUR7NC
43	88.5	7.1	1203	2 B55094
44	88.5	7.1	2954	2 T14156
45	88	7.1	505	2 S39520

ALIGNMENTS

RESULT 1

JC7517
caspase-14/a - human

C/Species: Homo sapiens (man)

C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

C/Accession: JC7517

R/Eckhart, L.; Ban, J.; Fischer, H.; Tschachler, E.

Biochem. Biophys. Res. Commun. 277, 655-659, 2000

A/Title: Caspase-14: Analysis of gene structure and mRNA expression during keratinocyt

A/Reference number: JC7517; PMID:20517231; PMID:11062009

A/Contents: Epidermal keratinocytes

A/Accession: JC7517

A/Molecule type: mRNA

A/Residues: 1-242 <ECK>

A/Cross-references: GB:AF097874

A/Comment: This enzyme accumulates during keratinocyte differentiation and is activate

A/Map position: 19p13.1

A/Introns: 9/3; 59/3; 135/1; 174/1; 208/3

C/Keywords: differentiation

Query Match 99.6%; Score 1234; DB 2; Length 242;

Best Local Similarity 99.6%; Pred. No. 1.2e-88;

Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLBEKKYMSGALALILCTKARSGSEDDALEHMPROLFEESTMRDPTAQ 60

DB 1 MSNPRSLBEKKYMSGARLALILCTKARSGSEDDALEHMPROLFEESTMRDPTAQ 60

QY 61 FOELEKFOQALDSREDPVSCAFVIMAHGRBGFLLGEDEGVYKLENIFFALNNKCOAL 120

DB 61 FOELEKFOQALDSREDPVSCAFVIMAHGRBGFLLGEDEGVYKLENIFFALNNKCOAL 120

QY 121 RARPKYIIIOACGEQRPDETVGSEIYVNIWIDSPOTITPYDIALHVSIVGSIYVRH 180

DB 121 RARPKYIIIOACGEQRPDETVGSEIYVNIWIDSPOTITPYDIALHVSIVGSIYVRH 180

QY 181 DQKSGCFIOTLVVFTFKKHILELLETVRRMAEALVOEGARKTNPEIGSTLRRLYL 240

DB 181 DQKSGCFIOTLVVFTFKKHILELLETVRRMAEALVOEGARKTNPEIGSTLRRLYL 240

QY 241 LQ 242

DB 241 LQ 242

QY 241 LQ 242

DB 241 LQ 242

QY 241 LQ 242

DB 241 LQ 242

QY 241 LQ 242

DB 241 LQ 242

QY 241 LQ 242

DB 241 LQ 242

QY 241 LQ 242

DB 241 LQ 242

QY 241 LQ 242

DB 241 LQ 242

QY 241 LQ 242

DB 241 LQ 242

QY 241 LQ 242

DB 241 LQ 242

QY 241 LQ 242

DB 241 LQ 242

C:Accession:J06507
R:Sato, N.; Mitsuiga, C.E.; Uchiyama, Y.; Oppenheim, R.W.
Gene 202, 127-132, 1997
A>Title: Cloning and expression of the cDNA encoding rat caspase-2.
A:Reference number: J06507; MUID:98087427; PMID:9427555
A:Accession: J06507
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-452 <S>A>
A:Cross-references: GB:U77933; NID:q2769705; PTD:AA969179.1. DT:07060706

Query Match	23.6%;	Score 293;	DB 2;	Length 458;
Best Local Similarity	31.5%;	Pred. No. 3e-15;		
Matches 75;	Conservative 52;	Mismatches 75;	Indels 36;	Gaps 7;

```

QY      25  REGSEBIDLALHEMFQALPKESTWAKDPALEOFOEELKFOQALDSREDPVSCAFVYLA      88
Db      219  RSGGDVHTTLVTLFKLIGNHVALYDQTAQMOEKLONFAQ-LPAHVDTSC-IVALLS      276
QY      89  HGREGFLKEDGEMVAKLENI,FEALNNKNGQALRAPKYIYLQACMGREDRG-----      140
Db      277  HVEGGIYGVDDGLDLOLQEVFLFDNANCPSLQNKPKAFILOACGSDTDGVDQDQGN      336
QY      141  -----BTVGDEIVAWIKDSPQTIPTTYTDALHVSTVEGYIAYRHDQKSCFIQTLV      192
Db      337  HAQSPCEBESDYGKEBELMKR-----LTPRSMICGYACLGNNAMRNTKGSYIEALT      391
QY      193  DVYTKR--KQHLELTETVRMAEALVEQEKAKTN-----PELQSTLRKLYL      241
Db      392  QVSEBACMVAHMDLVKNALIKS-----RSRYAAGTEHFHKCKEMSEVCSYTLCOQLY      445

```

```

RESULT 3
A54821
apoptosis regulator ICH-1, stimulatory form L - human
C:Species: Homo sapiens (man)
C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
C:Accession: A54821
C:Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Vian, J.
Cell 78, 739-750, 1994
A:Title: Ich-1, an Ice/ced-3-related gene, encodes both positive and negative regulators
A:Reference numbers: A54821; M01D:94373811; PMID:8087842

```

A; accession: A54821
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-435 <MNA>
A; Cross-references: GB:U13021; NID:g537291; PID:g537292
C; keywords: alternative splicing; apoptosis

	Query Match	23.3%	Score 289;	DB 2;	Length 435;
	Best Local Similarity	31.1%	Fred. No. 5.9e-15;		
	Matches	74;	Conservative 51;	Mismatches 17;	Indels 36; Gaps 7;
QY	29	RESEEDLDALAHMFQRLPEFSTWKRDPDTAEQFOEELKFOQADISREDPSCAFVYMA	88		
Db	202	RSQGDVHSTLVTLFKLTGGDVVHLCQDTAQEMQEKLNQFQ-LPAHVTBSC-IVALLIS	259		
QY	89	HGRGSEFKGEDGEMVEXKLENLFEALNNKCCQLRAKPKYITIQACGEQORDPQ-----	140		
Db	260	HGVAGALYGVQDKLLOEVHFOFLDPNNAKPSLQKPKMFLIQACGGETDGVQDQDKN	319		
QY	141	-----ETVGGDEIVWVWKDSFQITPTFYDAAIAHVSTVEGYIAYRRDQSGSCICTLV	192		
Db	320	HAGSPGCEESDAQKE-----KLPRGRLPTRSDMIQGVACLKGTAMNRNTRKGSWTEMLA	374		
QY	193	DVPEKRR--KSHITLLELVNRRMAEALVQEGKARKN-----PEIQSTLRKRLV	241		
Db	375	QVSRERCDNHVAMLVKVALIID---RGGVAPGTEFNRCKEMSEVCSLTICHLVY	428		

RESULT 4
JCS410
CPP32 protein - mouse

C.Species: Mus musculus (house mouse)
C.Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999
C.Accession: J05410
R.Mukasa, T.; Uraae, K.; Momoi, M.Y.; Kimura, I.; Momoi, T.
Biochem. Biophys. Res. Commun. 231, 770-774, 1997
Article: Specific expression of Cp32 in sensory neurons of mouse embryos and activatio
Reference number: J05410; MUID:97224429; PMID:9070890

A|Status: nucleic acid sequence not shown
A|Molecule type: mRNA
A|Residues: 1-277 <MDU>
A|Cross-references: DDBJ:D86352

A:Experimental source: embryo
C:Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons

Query Match	22.8%	Score 282.5;	DB 2;	Length 277;
Best Local Similarity	32.4%;	Pred. No. 1.1e-14;		
Matches 81;	Conservative 38;	Mismatches 104;	Indels 27;	Gaps 8;

```

QY      9 EEKYDMSGALALILCVT-----KAREGEEDLDAL EHNFRQIEFESTMKRDPTA 58
Db      34 DSSYKMDPEMGICIIITNNKFNFKSTGMSRSRGSDVDANLRREFEMGAEVRVRNKDITR 93

```

QY 59 ECGEELKEFOQALDSRDEPVSACFVVMAGHGEGFLXGDEGMVKENTLFEALNNKCO 118
 Db 94 EELMEINLDSVSKEDHKSRSFV---VLLSHGREGVITCTNGP-VDLKLTSPRGRGYA 146

QY 119 ALFAKEKYIIIOACRGEORDPG-ETVGDEIVWVIKDSFQILEPTDHALHVSTVEGYIA 177

Qb 150 SLTGKPKLEITIOACRGTELDGQIFETDSTENEFAC-----QKTVENRDTVYVYTAACVCS 205

```

QY      178 YAHDOKSCFIOTLVNDFVTKRGHILE--LITETVRMA---EAEIYQEGKARKTNPE 230
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      206 WENSKDSCSWETISICSMI-KTAAHKTETMHITITPYINPDTTTPSSSCCTDCCMHITKQITD 260
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

[illegible]

RESULT 5
S64710
Cysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster
C/Species: Crictetus griseus (Chinese hamster)
C/Date: 14-Feb-1997 #sequence_rev10 13-Mar-1997 #text_change 05-Nov-1999
C/Accession: S64710; S72395
R/Wang, X.; Zelenski, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.
EMBO J. 15, 1012-1020, 1996
A/Titles: Cleavage of steroid regulatory element binding proteins (SREBPs) by CPP32 during
A/Reference number: S64710; WIDB:96183185; PMID:8605870

A;/Accession: S6410
A;/Status: nucleic acid sequence not shown
A;/Molecule type: mRNA
A;/Residues: 1-277 <NAN>
A;/Cross-references: EMBL:U27463

R;Wang, X.
submitted to the EMBL Data Library, May 1995
A;Reference number: S72395

A:Accession: S72395
A:Molecule type: mRNA
A:Residues: 1-79, 'A', 81-146, 'Y', 148-277 (<N>)
A:Cross-references: EMBL:G127463; NID:G1244443; PIDD:AAB01511.1; PID:G1244444
A:Keywords: apoptosis; cysteine proteinase; hydrolysis

Query Match 22.6%; Score 280.5; DB 2; Length 277;
Best Local Similarity 35.9%; Pred. No. 1,6e-14;
Matches 79; Conservative 31; Mismatches 93; Totals 17; Cane 7.

[illegible]

```

Db      121 HGDEGVIPGTGDP-IDLKKLTSTYFGDRCSRSLIGPKFLFIQACGTLDCGIELTDSGTE 179
QY      148 IWMVTKDSPTPTPTDNLHVSTVEGYIAYRHDKGSCFIQTVADVETKRGHILE--- 204
Db      180 DDMTC---QKTPVADFLYAVSTAPGYISWNPDPDGSFIOSLCSML-KLYAHLEPMH 234
QY      205 LITEVTRMA---EAEIVQEGKARKNPEIQLSLRKLY 240
Db      235 ILTRVNRKVAETEFSEFSLDSTFHAKKQIPCIYVSMLTKEYL 274

```

RESULT 6
A55315
cysteine proteinase (EC 3.4.22.-) CPP32 precursor - human

N.Alternate names: cysteine proteinase CPP32
C.Species: Homo sapiens (man)
C.Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000
C.Accession: A55315; S58899; I39005
R.Fernandes-Alnemri, T.; Litwack, G.; Alnemri, E.S.
J. Biol. Chem. 269, 30761-30764, 1994
A.Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elegans
A.Reference number: A55315; MUID:95074098; PMID:7983002
A.Accession: A55315
A>Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-277 <PER>
A.Cross-references: GB:U13737; NID:9561665; PIDN:AAA65015.1; PID:9561666
R.Nicholson, D.M.; Ali, A.; Thornberry, N.A.; Vailancourt, J.P.; Ding, C.K.; Gallant, M.; Yu, V.L.; Miller, D.K.
Nature 376, 37-43, 1995
A.Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammalian
A.Reference number: S58899; MUID:95319529; PMID:7596430
A.Accession: S58899
A.Molecule type: protein
A.Residues: 29-46; 116-189, 'E', 191-193 <NIC>
R.Tewart, M.; Quan, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Poirier, Cell 81, 801-809, 1995
A.Title: Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease
A.Reference number: A56924; MUID:95292347; PMID:7774019
A.Accession: I39005
A>Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-189, 'E', 191-277 <RES>
A.Cross-references: EMBL:U26943; NID:9857568; PIDN:AAA74929.1; PID:9857569
C.Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query Match 22.0%; Score 272.5; DB 2; Length 277;
Best Local Similarity 31.9%; Pred. No. 6.5e-14;
Matches 80; Conservative 39; Mismatches 103; Indels 29; Gaps 9;

```

QY      9 EEKYDMSGALALILCVTK-----AREGSEEDLALHEMFRLRFESTMKRDPTA 58
Db      34 DNSYKMDYPRMGCTIINNNKHFKSTMTSRSGTDVAANLRETFRLKLEVRNKKDLTR 93
QY      59 EGFQSEIEKEQQAIDSRDPVSCAFVYVMAHGEGLKGDG--EWYKLENTLEALNNKN 116
Db      94 EELVELMRDYSKEDHSRSPFC---VLSHGEGGILFGNNGPVDLKKTNFF---RGDR 147
QY      117 QQLRAKPKYITIQACGEQDPPG-ELVGGDEIYMWIKDSPQITPTTDALHYSTVEGY 175
Db      148 CRSLTGKPKLFIQACGTEIDCGIETDSGVDDMAC---HKLPVADFLYAVSTAPGY 203
QY      176 IAYVHDGKSGCFIQTLDVPTK--RKGHILELLETVTRMA-EAEIVQ---EGARKTNP 229
Db      204 YSMWNSKDGWFIQSLCAMLKQYADKLEFMIILTRVNRKVAETEFSEFSPDITFAKKQIP 263
QY      230 EIOSTLRKRLY 240
Db      264 CIVSMLTKEYL 274

```

RESULT 7

```

JC7123
caspase-9 long chain - mouse
C.Species: Mus musculus (house mouse)
C.Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C.Accession: JC7123
R.Fujita, E.; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T.
Biochem. Biophys. Res. Commun. 264, 550-555, 1999
A.Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9
A.Reference number: JC7123; MUID:20001956; PMID:10529400
A.Accession: JC7123
A>Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-454 <FUJ>
A.Cross-references: DDBJ:AB019600; NID:96440941; PID:96440942

```

Query Match 21.3%; Score 264.5; DB 2; Length 454;
Best Local Similarity 30.6%; Pred. No. 4.9e-13;
Matches 76; Conservative 36; Mismatches 89; Indels 47; Gaps 7;

```

QY      29 REGSEEDLALHEMFRLRFESTMKRDPTAEQ---FQEELEKFOQAIDSRDPVSCAFV 84
Db      218 RFGSNIDRDKLEHRRFRMLRFVVEVKNLDLTAKKMTALMEMAHNRHPLD-----CFVY 270
QY      85 VIMAHGRE-----GFLKGEDENYKLENTLEALNNKNQALRAKPKYITIQACGEQD 137
Db      271 VILSHGCGASHIQFGAVVGTDCGVSITKYNINFGSCGCPGLGKPKLFIQACGGEQK 330
QY      136 D-----EGETVGGDEIYMWIK-----DSQITPTPTDNLHYSTVEGYI 176
Db      331 DNGFEVACTSGGRTLDSPEDATPFQGRPRPLDLDVAVSLFPSPDILVSYTFPGFV 390
QY      177 AYRHDKGSCFIQTVADVTK--RKGHILELLETVTRMAEAEIVQEGKARKNPEIQST 234
Db      391 SWRDKKSGSWYLETLDGILFQWARSBDLSILRV-----ANAVSEKGTQYQIPGCFNF 444
QY      235 LKKRLVLYQ 242
Db      445 LKKKLPFK 452

```

RESULT 8

A49429
interleukin-1 beta-converting enzyme homolog CED-3 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
C.Accession: A49429; T37312
R.Yuan, J.; Shaham, S.; Ledoux, S.; Ellis, H.M.; Horvitz, H.R.
Cell 75, 641-652, 1993
A.Title: The C. elegans cell death gene ced-3 encodes a protein similar to mammalian

A.Reference number: A49429; MUID:94061982; PMID:8242740
A.Accession: A49429
A>Status: preliminary
A.Molecule type: DNA
A.Residues: 1-503 <YUA>
A.Note: sequence extracted from NCBI backbone (NCBI:1.139825, NCBI:1.139826)
A>Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-417, 'R', 419-503 <YU2>
A.Cross-references: EMBL:129052; PIDN:AAA27982.1
C.Genetics:
A.Gene: ced-3
A.Intons: 45/3; 94/2; 179/1; 289/3; 361/1; 403/3; 483/3

Query Match 20.1%; Score 248.5; DB 2; Length 503;
Best Local Similarity 27.9%; Pred. No. 9.8e-12;
Matches 68; Conservative 42; Mismatches 93; Indels 41; Gaps 6;

```

QY      29 REGSEEDLALHEMFRLRFESTMKRDPTAEQFOEIEKEQQAIDSRDPVSCAFVYMA 88
Db      259 RNGTKADKDNLTNLFRCGAYTICKDNLTRGMILITIRDEAK---HSHSDSAIVLIS 314

```

QY 89 HGRBGLKGEDEGMVKNLFEALNNKNCQALRAKPKYIIIOACRGEORPGRTV----- 143
 Db 315 HGEENVILGVDDIPISTHEIYDILNANAPRLANKKIVFOACRGERNDGFPILDSVD 374
 QY 144 -----GGDEIVWVWDSP-----OTIFTYDALHVSIVTEGYTAJR 179
 Db 375 GVPAPLRRGMWN-----RDGPLENFGCVRPQVOQWMKKPSQADILLAVATTAQYVSWR 429
 QY 180 HDQKSGCFIQTLDVFT--KRKGHILELLEVTETVRMAEALVQSG-KARKTNPEIQSLR 236
 Db 430 NSAGSMFIQAVCEVFSTHAKMDVVELLITVNNKKVACGFTSGSNTLKQMPMTSRL 489
 QY 237 KRLTY 240
 Db 490 KKFY 493

RESULT 9

167437
 cysteine proteinase (EC 3.4.22.-) P32 - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
 C/Accession: I67437
 R/Flaws: J.A.: Kugu, K.; Tshovich, A.M.; Desanti, A.; Tilly, K.I.; Hirschfield, A.N.; Tili
 Endocrinology 136, 5042-5053, 1995
 A/Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cel
 nuloa cells of the ovarian follicle.
 A/Reference number: 153300; MUID:96042509; PMID:7588240
 A/Accession: I67437
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-212 <RFS>
 A/References: EMBL:U34685; NID:91004370; PIDN:AAC52261.1; PID:91004371
 C/Keywords: cysteine proteinase; hydrolase

Query Match 19.9%; Score 246.5; DB 2; Length 212;
 Best Local Similarity 31.5%; Pred. No. 5e-12;
 Matches 69; Conservative 34; Mismatches 89; Indels 27; Gaps 8;

QY 9 BEKYDMSGALALILCVT-----KAREGEEDLDALHEMFQOLRFESTMKDPTA 58
 Db 5 DSSYKMDPYEMGLCTIINKNFHKSCTGMSARNGTDVDAANLRETFMALKYEVANKKDLTR 64
 QY 59 EGFQEELEKFOQALDSREDPVSCAFVVLMAHGREGLKGEHGMVKNLELFEALNNKNCQ 118
 Db 65 EEIMEIMDSVSKEDHSKRSSFVC---VILSHGDEGVIFGNGP-VDLKLTLSFFRDYCR 120
 QY 119 ALRAKPKVITIOCRGEQDPG-ETVGG--DEIVMWIKDSPQTIPTYTDLHVSIVTEGY 175
 Db 121 SLTGKPKLEFIQACRGTELDGIRITDSGADDDVAC-----QKKPVEADFLVYSSAPGY 174
 QY 176 IAVRHQKSGCFIQTLDVFTKKRGHILE--LLEVTTR 211
 Db 175 YSWRNSRGSGSWFIQSLC-AMLKIVYAKHLEFMHILITRYNR 212

RESULT 10

G02635
 ICS-LAP6 - human
 C/Species: Homo sapiens (man)
 C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
 C/Accession: G02635
 R/Duan, H.; Orth, K.; Chinaiyan, A.M.; Poirier, G.G.; Froelich, C.J.; He, W.W.; Dixit,
 submitted to the EMBL Data Library, April 1996
 A/Reference number: H01513
 A/Accession: G02635
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-416 <DUA>
 A/Cross-references: EMBL:U56390; NID:91336026; PIDN:AAC50640.1; PID:91336027

Query Match 19.3%; Score 239.5; DB 2; Length 416;
 Best Local Similarity 28.7%; Pred. No. 3.9e-11;

Matches 72; Conservative 46; Mismatches 84; Indels 49; Gaps 9;
 QY 27 KAREGEEDLDALHEMFQOLRFESTMKDPTAEQFOELEKFOQALDSRED--PVSCAFV 84
 Db 178 RRTGSDNIDCEKLRRRSSLSHFVWVKGDLTAKKVALLEL-----ARQHGALDDCCV 232
 QY 85 VLMAHGNE-----GFLKGEDEGMVKNLELFEALNNKNCQALRAKPKYIIIOACRGEOR 137
 Db 233 VILSHGQASHLOPPGAVYGTGCGPVSVEKIVNIFNGTSCPSLGKPKLFIQACGGEQK 292
 QY 138 DPG-----ETVGG-----DEIVMWIKDSPQTIPTYTDLHVSIVT 171
 Db 293 DHGEFVASTPDEBSPSSNPEPDATPROEGLRTPDOL-----DAISSLPSTDIFFVAST 347
 QY 172 VEGYIAVRHQKSGCFIQTLDVFTKKRGHILELLEVTETVRMAEALVQSGKARKTNPEI 231
 Db 348 FPGFVSWRDPKSGSGWYETLIDIF-EQWAH-SEDLQSLLRVANAIVSK-GIYKQMPGC 403
 QY 232 QSTLRKRLTYQ 242
 Db 404 FNFLRKXLFK 414

RESULT 11

T20038
 hypothetical protein C48D1.2 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C/Accession: T20038
 R/Burton, J.
 submitted to the EMBL Data Library, October 1996

A/Reference number: Z19214
 A/Accession: T20038
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-495 <WIL>
 A/Cross-references: EMBL:Z81049; PIDN:CAB02848.1; GSPDB:GN00022; CESP:C48D1.2
 C/Experimental source: clone C48D1
 A/Genes: CESP:C48D1.2
 A/Map position: 4
 A/Intons: 44/3; 93/2; 178/1; 288/3; 360/1; 402/3; 466/1

Query Match 18.6%; Score 230; DB 2; Length 495;
 Best Local Similarity 27.6%; Pred. No. 2.6e-10;
 Matches 60; Conservative 39; Mismatches 78; Indels 40; Gaps 5;

QY 29 PRGSEEDLDALHEMFQOLRFESTMKDPTAEQFOELEKFOQALDSREDPVSCAFVILMA 88
 Db 258 RNGTAKDXNLNINFRCKGYTVCNDLITRGKMLTTRDPAK---HESHGSAIIVITIS 313
 QY 89 HGRBGLKGEDEGMVKNLELFEALNNKNCQALRAKPKYIIIOACRGEORPGRTV----- 143
 Db 314 HGEENVILGVDDIPISTHEIYDILNANAPRLANKKIVFOACRGERNDGFPILDSVD 373
 QY 144 -----GGDEIVWVWDSP-----OTIFTYDALHVSIVTEGYTAJR 179
 Db 374 GVPAPLRRGMWN-----RDGPLENFGCVRPQVOQWMKKPSQADILLAVATTAQYVSWR 428
 QY 180 HDQKSGCFIQTLDVFT--KRKGHILELLEVTETVRMA 214
 Db 429 NSAGSMFIQAVCEVFSTHAKMDVVELLITVNNKKYA 465

RESULT 12

B56084
 interleukin-1beta converting enzyme gamma isozyne - human
 C/Species: Homo sapiens (man)
 C/Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
 C/Accession: B56084
 R/Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
 J. Biol. Chem. 270, 4312-4317, 1995
 A/Title: Cloning and expression of four novel isoforms of human interleukin-1beta conver

A;Reference number: A56084; MUID:95181414; PMID:7876192
A;Accession: B56084
A>Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-311 <ALN>
A;Cross-references: GB:U13698; NID:g717041; PIDN:AAC50108.1; PID:g717042
C;Genetics:
A;Gene: IL1BCE
C;Keywords: alternative splicing

Query Match 18.2%; Score 226; DB 2; Length 311;
Best Local Similarity 29.5%; Pred. No. 3..1e-10;
Matches 77; Conservative 41; Mismatches 89; Indels 54; Gaps 12;

Dy 15 SGAMALLILCVTK-----AREGSEEDLDLEHMFROLFRESYMKRDPPTAEQFQELERKQ 69
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Db SRTRLALLICNEEFDSIPRRTGAEVDITGMILLONIGSVDVYKANLITASDTELEAF 126
70 QAIIDREDPVSCAFVYLMAHG-RREGFLKGDEGVN---XLENLFEALNNKNCOALRAKP 124
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Dy 125 KYVIIQACRGQRDPGEETIVMYIKDS-----PQTIIPTYTDAL--HV---- 168
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Db 139 HRPHEKTS--DSTFLVMSHGIRGICGKHSEQVPDILQNALIFMNLINYNCPSELKDKP 184
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Dy 169 ---YSTVEGYIAVRHDQKSGCFIQLTVDFYTRKRGHILEL-----LTEYTRMAEALVQ 220
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RESULT 13
A56084
interleukin-beta converting enzyme beta isozyme - human
C;Species: Homo sapiens (man)
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
C;Accession: A56084
R;Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
J. Biol. Chem. 270, 4312-4317, 1995
A;Title: Cloning and expression of four novel isoforms of human interleukin-beta conver
A;Reference number: A56084; MUID:95181414; PMID:7876192
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A>Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-383 <ALN>
A;Cross-references: GB:U13697; NID:g717039; PIDN:AAC50107.1; PID:g717040
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A;Gene: IL1BCE
C;Keywords: alternative splicing

Query Match 18.2%; Score 226; DB 2; Length 383;
Best Local Similarity 29.5%; Pred. No. 3..9e-10;
Matches 77; Conservative 41; Mismatches 89; Indels 54; Gaps 12;

Dy 15 SGAMALLILCVTK-----AREGSEEDLDLEHMFROLFRESYMKRDPPTAEQFQELERKQ 69
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		Cispecies: Homo sapiens (man)		
		C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999		
		C/Accession: A54267; A42677; S21734; S24164		
		R/Cerretti, D.P.; Hollingsworth, L.T.; Kozlosky, C.J.; Valentine, M.B.; Shapiro, D.N.; Genomics 20, 468-473, 1994		
		A>Title: Molecular characterization of the gene for human interleukin-1beta converting		
		A/Reference number: A54263; MUID:94307734; PMID:8034320		
		A/Accession: A54263		
		A>Status: preliminary; not compared with conceptual translation		
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		A/Cross-references: GB:L27475		
		R/Cerretti, D.P.; Kozlosky, C.J.; Mosley, B.; Nelson, N.; Van Ness, K.; Greenstreet, T		
		Science 256, 97-100, 1992		
		A>Title: Molecular cloning of the interleukin-1beta converting enzyme.		
		A/Reference number: A42677; MUID:92229430; PMID:1373520		
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		A>Status: preliminary		
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		A/Cross-references: GB:M87507; NID:9435598; PIDN:AA66942.1; PID:9186286		
		R/Thornberry, N.A.; Bull, H.G.; Calafsky, J.R.; Chapman, K.T.; Howard, A.D.; Kostura, M		
		J.; Ding, G.J.F.; Egger, L.A.; Gaffney, E.P.; Limjoco, G.; Palyha, O.C.; Raju, S.M.; Ro		
		ccl, M.J.		
		Nature 356, 768-774, 1992		
		A>Title: A novel heterodimeric cysteine protease is required for interleukin-1beta proc		
		A/Reference number: S21734; MUID:92244338; PMID:1574116		
		A/Accession: S21734		
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		A/Cross-references: EMBL:X65019; NID:933792; PIDN:CMA46153.1; PID:933793		
		R/Kronheim, S.R.; Muma, A.; Greenstreet, T.; Glackin, P.J.; van Ness, K.; March, C.J.		
		Arch. Biochem. Biophys. 296, 698-703, 1992		
		A>Title: Purification of interleukin-1beta converting enzyme, the protease that cleave		
		A/Reference number: S24164; MUID:92337439; PMID:1321594		
		A/Accession: S24164		
		A>Status: preliminary		
		A/Molecule type: protein		
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		A/Gene: GDB:IL1BC		
		A/Cross-references: GDB:132368; OMIM:147678		
		A/Map position: 11q23-11q23		
		C/Keywords: cysteine proteinase; hydrolase		
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		Best local Similarity	29.5%;	Pred. No. 4.2e-10;
		Matches	77; Conservative	41; Mismatches 89; Indels 54; Gaps 12;
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Oy		125	KVIYIQCRGEQRDPGETVGDELIVMYIKS-----PQIIPYTDLA---HV----	168
Dd		278	KVIIIIQCRGD--SPG-----VVWFKDSGVGSGLSLPTBEFDADIKKAHIKDGF	327
Oy		169	--YSTVEGYAVYHRDKSGSCFIOTLVDFVTKRGHILET-----LFEVTRMAAEILVQ	220

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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:50:22 ; Search time 59.5 Seconds
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1268.642 Million cell updates/sec

Title: US-10-068-564-5

Perfect score: 1239
Sequence: 1 MSNPRSLBEKKYMSGALA.....KARKTNPISQTLKRLYLQ 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1279676 seqs, 311918243 residues

Total number of hits satisfying chosen parameters: 1279676

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1239	100.0	242	9 US-09-989-903-5	Sequence 5, Appl1
2	1239	100.0	242	14 US-10-068-564-5	Sequence 5, Appl1
3	1234	99.6	242	9 US-09-845-028-2	Sequence 2, Appl1
4	1234	99.6	242	10 US-09-851-873-105	Sequence 105, App
5	1234	99.6	242	15 US-10-114-432-3	Sequence 3, Appl1
6	1234	99.6	242	15 US-10-114-432-15	Sequence 15, Appl1
7	1234	99.6	242	15 US-10-114-432-17	Sequence 17, Appl1
8	1234	99.6	242	15 US-10-114-432-18	Sequence 18, Appl1
9	1234	99.6	242	15 US-10-114-432-26	Sequence 26, Appl1
10	1234	99.6	242	15 US-10-114-432-27	Sequence 27, Appl1
11	1234	99.6	242	15 US-10-114-432-28	Sequence 28, Appl1
12	1234	99.6	242	15 US-10-114-432-30	Sequence 30, Appl1
13	1234	99.6	242	15 US-10-114-432-31	Sequence 31, Appl1
14	1234	99.6	242	15 US-10-114-432-67	Sequence 67, Appl1
15	1234	99.6	242	15 US-10-114-432-69	Sequence 69, Appl1

16	1234	99.6	242	15 US-10-114-432-71	Sequence 71, Appl1
17	1234	99.6	242	15 US-10-114-432-73	Sequence 73, Appl1
18	1232	99.4	242	15 US-10-114-432-13	Sequence 13, Appl1
19	1232	99.4	242	15 US-10-114-432-23	Sequence 23, Appl1
20	1229	99.2	241	15 US-10-114-432-37	Sequence 37, Appl1
21	1222	98.6	242	15 US-10-114-432-11	Sequence 11, Appl1
22	1222	98.6	242	15 US-10-114-432-22	Sequence 22, Appl1
23	1200	96.9	241	15 US-10-114-432-36	Sequence 36, Appl1
24	1200	96.9	321	15 US-10-114-432-21	Sequence 21, Appl1
25	1200	96.9	321	15 US-10-114-432-66	Sequence 66, Appl1
26	1200	96.9	321	15 US-10-114-432-72	Sequence 72, Appl1
27	1200	96.9	321	15 US-09-764-803A-24	Sequence 24, Appl1
28	1194	96.4	242	9 US-09-845-028-9	Sequence 9, Appl1
29	1189	96.0	229	9 US-09-764-803A-4	Sequence 9, Appl1
30	1166	94.1	229	9 US-09-989-903-9	Sequence 9, Appl1
31	1065	86.0	214	14 US-10-068-564-9	Sequence 29, Appl1
32	934.5	75.4	253	15 US-10-114-432-29	Sequence 2, Appl1
33	934.5	75.4	257	9 US-09-764-803A-2	Sequence 2, Appl1
34	934.5	75.4	260	14 US-10-068-564-2	Sequence 34, Appl1
35	934.5	75.4	260	14 US-10-114-432-34	Sequence 7, Appl1
36	890	71.8	230	9 US-09-989-903-7	Sequence 7, Appl1
37	890	71.8	230	14 US-10-068-564-7	Sequence 5, Appl1
38	890	71.8	230	15 US-10-114-432-5	Sequence 19, Appl1
39	890	71.8	230	15 US-10-114-432-19	Sequence 64, Appl1
40	890	71.8	230	15 US-10-114-432-68	Sequence 35, Appl1
41	890	71.8	230	15 US-10-114-432-35	Sequence 32, Appl1
42	890	71.8	230	15 US-10-114-432-35	
43	890	71.8	185	15 US-10-114-432-35	
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ALIGNMENTS

RESULT 1
US-09-989-903-5
; Sequence 5, Application US/09989903
; Patent No. US20020146804A1
; GENERAL INFORMATION:
; APPLICANT: Alnemuri, Emad S.
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434D1
; CURRENT APPLICATION NUMBER: US/09/989,903
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-989-903-5

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Best Local Similarity 100.0%; Pred. No. 1.3e+113; Indels 0; Gaps 0;
Matches 242; Conservative 0; Mismatches 0;
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DB 121 RAKPKYITIOACGEGQRPBETVGGDEIVWIDSPOTITPYTDALHVSIVBEGYIAYRH 180
QY 181 DOKGSCFIOTLVVFTFKRKSHIELLTVTRNAEELVQEGARKTNPISQTLKRLYL 240
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Db 241 LQ 242

RESULT 2

US-10-068-564-5
; Sequence 5, Application US/10068564
; Publication No. US20030040096A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emed S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C2
; CURRENT APPLICATION NUMBER: US/10/068,564
; CURRENT FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 242
; TYPE: PRF
; ORGANISM: Homo sapien
US-10-068-564-5

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Best Local Similarity 100.0%; Pred. No. 1,3e-113;

Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

US-09-845-028-2
; Sequence 2, Application US/09845028
; Patent No. US20020081705A1
; GENERAL INFORMATION:
; APPLICANT: Mankovich, John
; TITLE OF INVENTION: HUMAN CASPASE-14 COMPOSITIONS
; FILE REFERENCE: BBI-111
; CURRENT APPLICATION NUMBER: US/09/845,028
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/199,962
; NUMBER OF SEQ ID NOS: 9
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; ORGANISM: Homo sapiens
US-09-845-028-2

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Best Local Similarity 99.6%; Pred. No. 4.1e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 241 LQ 242

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US-09-851-873-105
; Sequence 105, Application US/09851873
; Publication No. US20030165488A1
; GENERAL INFORMATION:
; APPLICANT: Kleitzi, Rolf F
; APPLICANT: Reardon, Ilene M
; TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
; FILE REFERENCE: 28341/00233
; CURRENT APPLICATION NUMBER: US/09/851,873
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 242
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-851-873-105

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RESULT 5

US-10-114-432-3
; Sequence 3, Application US/10114432
; Publication No. US20040019915A1

GENERAL INFORMATION:
APPLICANT: Challita-Eld, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobivits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
TITLE OF INVENTION: DETECTION OF CANCER
FILE REFERENCE: 51158-20066.00
CURRENT APPLICATION NUMBER: US/10/114,432
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 242
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-114-432-3

Query Match 99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 4.1e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 FOEELKFOAIDSREDPVSCAFVVLMAHGREBFLKGEDEGEMVKLENLFEALNNKCOAL 120
DB 61 FOEELKFOAIDSREDPVSCAFVVLMAHGREBFLKGEDEGEMVKLENLFEALNNKCOAL 120
QY 121 RAKPKYIIIOACRGDRPGEIVGDEIVWIKOSPOTIPYTDALHYSTVEGYIAYRH 180
DB 121 RAKPKYIIIOACRGDRPGEIVGDEIVWIKOSPOTIPYTDALHYSTVEGYIAYRH 180
QY 181 DOKGSCFIQTLVDVFTFKRGHILELLEVTTRMAEAEIVOGSKARKTNPEIOSTLRKRLY 240
DB 181 DOKGSCFIQTLVDVFTFKRGHILELLEVTTRMAEAEIVOGSKARKTNPEIOSTLRKRLY 240
QY 241 LQ 242
DB 241 LQ 242

RESULT 6
US-10-114-432-15
Sequence 15, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:

APPLICANT: Challita-Eld, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobivits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
TITLE OF INVENTION: DETECTION OF CANCER
FILE REFERENCE: 51158-20066.00
CURRENT APPLICATION NUMBER: US/10/114,432
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 242
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-114-432-15

Query Match 99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 4.1e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRLSEEEKYDMSGALALILCVTKAREGSEEDLDALHMFRLRPESTMKRDPATAQ 60
DB 1 MSNPRLSEEEKYDMSGARLALLICVTKAREGSEEDLDALHMFRLRPESTMKRDPATAQ 60
QY 61 FOEELKFOAIDSREDPVSCAFVVLMAHGREBFLKGEDEGEMVKLENLFEALNNKCOAL 120
DB 61 FOEELKFOAIDSREDPVSCAFVVLMAHGREBFLKGEDEGEMVKLENLFEALNNKCOAL 120
QY 121 RAKPKYIIIOACRGDRPGEIVGDEIVWIKOSPOTIPYTDALHYSTVEGYIAYRH 180
DB 121 RAKPKYIIIOACRGDRPGEIVGDEIVWIKOSPOTIPYTDALHYSTVEGYIAYRH 180
QY 181 DOKGSCFIQTLVDVFTFKRGHILELLEVTTRMAEAEIVOGSKARKTNPEIOSTLRKRLY 240
DB 181 DOKGSCFIQTLVDVFTFKRGHILELLEVTTRMAEAEIVOGSKARKTNPEIOSTLRKRLY 240
QY 241 LQ 242
DB 241 LQ 242

RESULT 7
US-10-114-432-17
Sequence 17, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:
APPLICANT: Challita-Eld, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobivits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
TITLE OF INVENTION: DETECTION OF CANCER
FILE REFERENCE: 51158-20066.00
CURRENT APPLICATION NUMBER: US/10/114,432
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 242
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-114-432-17

Query Match 99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 4.1e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRLSEEEKYDMSGALALILCVTKAREGSEEDLDALHMFRLRPESTMKRDPATAQ 60
DB 1 MSNPRLSEEEKYDMSGARLALLICVTKAREGSEEDLDALHMFRLRPESTMKRDPATAQ 60
QY 61 FOEELKFOAIDSREDPVSCAFVVLMAHGREBFLKGEDEGEMVKLENLFEALNNKCOAL 120
DB 61 FOEELKFOAIDSREDPVSCAFVVLMAHGREBFLKGEDEGEMVKLENLFEALNNKCOAL 120
QY 121 RAKPKYIIIOACRGDRPGEIVGDEIVWIKOSPOTIPYTDALHYSTVEGYIAYRH 180
DB 121 RAKPKYIIIOACRGDRPGEIVGDEIVWIKOSPOTIPYTDALHYSTVEGYIAYRH 180
QY 181 DOKGSCFIQTLVDVFTFKRGHILELLEVTTRMAEAEIVOGSKARKTNPEIOSTLRKRLY 240
DB 181 DOKGSCFIQTLVDVFTFKRGHILELLEVTTRMAEAEIVOGSKARKTNPEIOSTLRKRLY 240
QY 241 LQ 242
DB 241 LQ 242

Db 241 LQ 242

RESULT 8
US-10-114-432-18
; Sequence 18, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-18

Query Match 99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 4.1e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLSEEEKYMSGALALLICVTKARSGSEEDLDALHMFRLRFESTMKRDPPTAEQ 60
|||
Db 1 MSNPRSLSEEEKYMSGARLALLICVTKARSGSEEDLDALHMFRLRFESTMKRDPPTAEQ 60
|||
QY 61 FOEELKFOQALDSREDPVSCAFVVLMAHGREGFLKGEDEGEMVKLENLFEALNNKCOAL 120
|||
Db 61 FOEELKFOQALDSREDPVSCAFVVLMAHGREGFLKGEDEGEMVKLENLFEALNNKCOAL 120
|||
QY 121 RAKPKYIIIOACGGEORDPGEIVGDEIWMVVKDSPTIPTYTDALHYSTVEGYIAYRH 180
|||
Db 121 RAKPKYIIIOACGGEORDPGEIVGDEIWMVVKDSPTIPTYTDALHYSTVEGYIAYRH 180
|||
QY 181 DQKSGCFIOTLVDFPKRGHILLETVTNRMAEALVQEGARKTNPEIOSTLRKRLY 240
|||
Db 181 DQKSGCFIOTLVDFPKRGHILLETVTNRMAEALVQEGARKTNPEIOSTLRKRLY 240
|||
QY 241 LQ 242
|||
Db 241 LQ 242

RESULT 9
US-10-114-432-26
; Sequence 26, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-26

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-26

Query Match 99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 4.1e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLSEEEKYMSGALALLICVTKARSGSEEDLDALHMFRLRFESTMKRDPPTAEQ 60
|||
Db 1 MSNPRSLSEEEKYMSGARLALLICVTKARSGSEEDLDALHMFRLRFESTMKRDPPTAEQ 60
|||
QY 61 FOEELKFOQALDSREDPVSCAFVVLMAHGREGFLKGEDEGEMVKLENLFEALNNKCOAL 120
|||
Db 61 FOEELKFOQALDSREDPVSCAFVVLMAHGREGFLKGEDEGEMVKLENLFEALNNKCOAL 120
|||
QY 121 RAKPKYIIIOACGGEORDPGEIVGDEIWMVVKDSPTIPTYTDALHYSTVEGYIAYRH 180
|||
Db 121 RAKPKYIIIOACGGEORDPGEIVGDEIWMVVKDSPTIPTYTDALHYSTVEGYIAYRH 180
|||
QY 181 DQKSGCFIOTLVDFPKRGHILLETVTNRMAEALVQEGARKTNPEIOSTLRKRLY 240
|||
Db 181 DQKSGCFIOTLVDFPKRGHILLETVTNRMAEALVQEGARKTNPEIOSTLRKRLY 240
|||
QY 241 LQ 242
|||
Db 241 LQ 242

RESULT 10
US-10-114-432-27
; Sequence 27, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-27

Query Match 99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 4.1e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLSEEEKYMSGALALLICVTKARSGSEEDLDALHMFRLRFESTMKRDPPTAEQ 60
|||
Db 1 MSNPRSLSEEEKYMSGARLALLICVTKARSGSEEDLDALHMFRLRFESTMKRDPPTAEQ 60
|||
QY 61 FOEELKFOQALDSREDPVSCAFVVLMAHGREGFLKGEDEGEMVKLENLFEALNNKCOAL 120
|||
Db 61 FOEELKFOQALDSREDPVSCAFVVLMAHGREGFLKGEDEGEMVKLENLFEALNNKCOAL 120
|||
QY 121 RAKPKYIIIOACGGEORDPGEIVGDEIWMVVKDSPTIPTYTDALHYSTVEGYIAYRH 180
|||
Db 121 RAKPKYIIIOACGGEORDPGEIVGDEIWMVVKDSPTIPTYTDALHYSTVEGYIAYRH 180
|||
QY 181 DQKSGCFIOTLVDFPKRGHILLETVTNRMAEALVQEGARKTNPEIOSTLRKRLY 240
|||
Db 181 RAKPKYIIIOACGGEORDPGEIVGDEIWMVVKDSPTIPTYTDALHYSTVEGYIAYRH 180
|||

QY 181 DQKSGCFIQTIVDFVTKRKHILLETVTTRMAEALVQSGKARKTNPEIQTIRKRLY 240
 DB 181 DQKSGCFIQTIVDFVTKRKHILLETVTTRMAEALVQSGKARKTNPEIQTIRKRLY 240
 QY 241 LQ 242
 DB 241 LQ 242

RESULT 11
 US-10-114-432-28
 ; Sequence 28, Application US/10114432
 ; Publication No. US20040019915A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chailita-Bid, Pia M.
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Morrison, Robert K.
 ; APPLICANT: Ge, Mangmao
 ; APPLICANT: Jakobivits, Aya
 ; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
 ; TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
 ; FILE REFERENCE: 51158-20066.00
 ; CURRENT APPLICATION NUMBER: US/10/114,432
 ; CURRENT FILING DATE: 2002-04-01
 ; NUMBER OF SEQ ID NOS: 88
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 28
 ; LENGTH: 242
 ; TYPE: PRF
 ; ORGANISM: Homo Sapiens
 US-10-114-432-28

Query Match 99.6%; Score 1234; DB 15; Length 242;
 Best Local Similarity 99.6%; Pred. No. 4.1e-113;
 Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLIEBKYMGSALALILCVTKARSGSEEDLDALHMFRLQRFESTMKRDPPTAEQ 60
 DB 1 MSNPRSLIEBKYMGSALALILCVTKARSGSEEDLDALHMFRLQRFESTMKRDPPTAEQ 60
 QY 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDEGEMVKLENTFEALNNKCOAL 120
 DB 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDEGEMVKLENTFEALNNKCOAL 120
 QY 121 RAKPKYIIOACRGORPGEVGDDEIVMVIKDSPTIPTYDHALHVSTVEGYIAYRH 180
 DB 121 RAKPKYIIOACRGORPGEVGDDEIVMVIKDSPTIPTYDHALHVSTVEGYIAYRH 180
 QY 181 DQKSGCFIQTIVDFVTKRKHILLETVTTRMAEALVQSGKARKTNPEIQTIRKRLY 240
 DB 181 DQKSGCFIQTIVDFVTKRKHILLETVTTRMAEALVQSGKARKTNPEIQTIRKRLY 240
 QY 241 LQ 242
 DB 241 LQ 242

RESULT 12
 US-10-114-432-30
 ; Sequence 30, Application US/10114432
 ; Publication No. US20040019915A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chailita-Bid, Pia M.
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Morrison, Robert K.
 ; APPLICANT: Ge, Mangmao
 ; APPLICANT: Jakobivits, Aya

;; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
 ;; TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
 ;; FILE REFERENCE: 51158-20066.00
 ;; CURRENT APPLICATION NUMBER: US/10/114,432
 ;; CURRENT FILING DATE: 2002-04-01
 ;; NUMBER OF SEQ ID NOS: 88
 ;; SOFTWARE: FastSeq for Windows Version 4.0
 ;; SEQ ID NO 30
 ;; LENGTH: 242
 ;; TYPE: PRF
 ;; ORGANISM: Homo Sapiens
 US-10-114-432-30

Query Match 99.6%; Score 1234; DB 15; Length 242;
 Best Local Similarity 99.6%; Pred. No. 4.1e-113;
 Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLIEBKYMGSALALILCVTKARSGSEEDLDALHMFRLQRFESTMKRDPPTAEQ 60
 DB 1 MSNPRSLIEBKYMGSALALILCVTKARSGSEEDLDALHMFRLQRFESTMKRDPPTAEQ 60
 QY 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDEGEMVKLENTFEALNNKCOAL 120
 DB 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDEGEMVKLENTFEALNNKCOAL 120
 QY 121 RAKPKYIIOACRGORPGEVGDDEIVMVIKDSPTIPTYDHALHVSTVEGYIAYRH 180
 DB 121 RAKPKYIIOACRGORPGEVGDDEIVMVIKDSPTIPTYDHALHVSTVEGYIAYRH 180
 QY 181 DQKSGCFIQTIVDFVTKRKHILLETVTTRMAEALVQSGKARKTNPEIQTIRKRLY 240
 DB 181 DQKSGCFIQTIVDFVTKRKHILLETVTTRMAEALVQSGKARKTNPEIQTIRKRLY 240
 QY 241 LQ 242
 DB 241 LQ 242

RESULT 13
 US-10-114-432-31
 ; Sequence 31, Application US/10114432
 ; Publication No. US20040019915A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chailita-Bid, Pia M.
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Morrison, Robert K.
 ; APPLICANT: Ge, Mangmao
 ; APPLICANT: Jakobivits, Aya
 ; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
 ; TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
 ; FILE REFERENCE: 51158-20066.00
 ; CURRENT APPLICATION NUMBER: US/10/114,432
 ; CURRENT FILING DATE: 2002-04-01
 ; NUMBER OF SEQ ID NOS: 88
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 31
 ; LENGTH: 242
 ; TYPE: PRF
 ; ORGANISM: Homo Sapiens
 US-10-114-432-31

Query Match 99.6%; Score 1234; DB 15; Length 242;
 Best Local Similarity 99.6%; Pred. No. 4.1e-113;
 Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLIEBKYMGSALALILCVTKARSGSEEDLDALHMFRLQRFESTMKRDPPTAEQ 60
 DB 1 MSNPRSLIEBKYMGSALALILCVTKARSGSEEDLDALHMFRLQRFESTMKRDPPTAEQ 60

```

QY 61 FOEELKFOQAIIDSRDVPSCAFVVLMAHGREGLKGEDEMGVLENTFEALNNKNCQAL 120
DB 61 FOEELKFOQAIIDSRDVPSCAFVVLMAHGREGLKGEDEMGVLENTFEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGQRDPGETVGGDEIVWIKDSPTIIPYTDALHYSTVEGYIAYRH 180
DB 121 RAKPKVYIIQACRGQRDPGETVGGDEIVWIKDSPTIIPYTDALHYSTVEGYIAYRH 180
QY 181 DQKGSCTIQLTVDFVTKRKGHILELLETVTRMAEAELVQEGKARKTNPEIOSTLRKRLY 240
DB 181 DQKGSCTIQLTVDFVTKRKGHILELLETVTRMAEAELVQEGKARKTNPEIOSTLRKRLY 240
QY 241 LQ 242
DB 241 LQ 242

```

RESULT 14

```

US-10-114-432-67
; Sequence 67, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Mangmao
; APPLICANT: Jakobivics, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: DETECTED 213PFI1 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-2006.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-67

```

```

Query Match 99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 4.1e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 MSNPRSLSEEEKYMGSAALALILICVTKARBSSEEDLDALHMFROLRFESTMKRDPTAQ 60
DB 1 MSNPRSLSEEEKYMGSAALALILICVTKARBSSEEDLDALHMFROLRFESTMKRDPTAQ 60
QY 61 FOEELKFOQAIIDSRDVPSCAFVVLMAHGREGLKGEDEMGVLENTFEALNNKNCQAL 120
DB 61 FOEELKFOQAIIDSRDVPSCAFVVLMAHGREGLKGEDEMGVLENTFEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGQRDPGETVGGDEIVWIKDSPTIIPYTDALHYSTVEGYIAYRH 180
DB 121 RAKPKVYIIQACRGQRDPGETVGGDEIVWIKDSPTIIPYTDALHYSTVEGYIAYRH 180
QY 181 DQKGSCTIQLTVDFVTKRKGHILELLETVTRMAEAELVQEGKARKTNPEIOSTLRKRLY 240
DB 181 DQKGSCTIQLTVDFVTKRKGHILELLETVTRMAEAELVQEGKARKTNPEIOSTLRKRLY 240
QY 241 LQ 242
DB 241 LQ 242

```

```

RESULT 15
US-10-114-432-69
; Sequence 69, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Mangmao
; APPLICANT: Jakobivics, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: DETECTED 213PFI1 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-2006.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-69

```

```

Query Match 99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 4.1e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 MSNPRSLSEEEKYMGSAALALILICVTKARBSSEEDLDALHMFROLRFESTMKRDPTAQ 60
DB 1 MSNPRSLSEEEKYMGSAALALILICVTKARBSSEEDLDALHMFROLRFESTMKRDPTAQ 60
QY 61 FOEELKFOQAIIDSRDVPSCAFVVLMAHGREGLKGEDEMGVLENTFEALNNKNCQAL 120
DB 61 FOEELKFOQAIIDSRDVPSCAFVVLMAHGREGLKGEDEMGVLENTFEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGQRDPGETVGGDEIVWIKDSPTIIPYTDALHYSTVEGYIAYRH 180
DB 121 RAKPKVYIIQACRGQRDPGETVGGDEIVWIKDSPTIIPYTDALHYSTVEGYIAYRH 180
QY 181 DQKGSCTIQLTVDFVTKRKGHILELLETVTRMAEAELVQEGKARKTNPEIOSTLRKRLY 240
DB 181 DQKGSCTIQLTVDFVTKRKGHILELLETVTRMAEAELVQEGKARKTNPEIOSTLRKRLY 240
QY 241 LQ 242
DB 241 LQ 242

```

Search completed: July 12, 2004, 14:04:00
Job time : 60.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:39:36 / Search time 72 Seconds
(without alignments)
949.674 Million cell updates/sec

Title: US-10-068-564-5
Perfect score: 1239
Sequence: 1 MSNPRLSEEXYDMSGALA.....KARKTNPRIQSTLRKRLYLQ 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_29Jan04:*
2: geneseqp180s:*
3: geneseqp190s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	ID	Description
1	1234	99.6	242	3	AAY93214 Amino aci
2	1234	99.6	242	5	AAG77980 Full-leng
3	1189	96.0	242	5	AAG77984 Full-leng
4	1166	94.1	229	3	AAY68865 Amino aci
5	1065	86.0	214	3	AAY93216 Amino aci
6	934.5	75.4	257	3	AAY68864 Amino aci
7	934.5	75.4	281	3	AAM93592 Mouse cas
8	934.5	75.4	281	3	AAY93213 Amino aci
9	890	71.8	230	3	AAY93215 Amino aci
10	472.5	38.1	234	5	AAY72882 Human asp
11	472.5	38.1	398	5	ABG76499 DNA encod
12	295	23.8	452	5	ABD10110 Mouse cas
13	293	23.6	452	7	ABD79812 Rat caspa
14	293	23.6	452	7	ADBE63000 Rat Prote
15	289	23.3	435	2	AAR66771 Human int
16	289	23.3	435	2	AAR98462 Human Ice
17	289	23.3	435	2	AAR90703 Interleuk
18	289	23.3	435	2	AAR26274 Cell deat
19	289	23.3	435	2	AAY21716 Amino ich
20	289	23.3	435	2	AAB14257 Human cas
21	289	23.3	435	4	AAB00599 Human cas
22	289	23.3	435	5	ABB78321 Amino aci
23	289	23.3	435	5	ABO1217 Human cas
24	289	23.3	435	7	ADBE63002 Human pro
25	289	23.3	441	2	AAR66768 Human int

26	289	23.3	441	3	AAB14253 Human Ich
27	280	22.6	245	4	AAB59579 Human cas
28	279.5	22.6	277	7	ADBE63080 Rat Prote
29	278.5	22.5	277	2	AAM47089 Rat inter
30	276	22.3	261	4	AAE00610 Chimeric
31	275	22.2	435	3	AAB14262 Mutant hu
32	274.5	22.2	277	4	AAG78712 Pig caspa
33	273.5	22.1	249	3	AAB26763 Human cas
34	273.5	22.1	277	2	AAW00372 Apopain C
35	273.5	22.1	277	2	AAR95831 Human int
36	273.5	22.1	277	2	AAR95831 Pro-Yama
37	273.5	22.1	277	2	AAW41688 Amino aci
38	273.5	22.1	277	2	AAW05395 Mouse cas
39	273.5	22.1	277	6	AAU05395 Bacteriop
40	273.5	22.1	277	7	ADD25641 Binding d
41	273	22.0	457	4	AAW25766 Human pro
42	272.5	22.0	277	4	AAW16600 Apopain C
43	272.5	22.0	277	2	AAY21717 Amino aci
44	272.5	22.0	277	4	AAU05394 Human cas
45	272.5	22.0	277	4	AAE00600 Human cas

ALIGNMENTS

RESULT 1
ID AAY93214 standard; protein; 242 AA.

XX AAY93214; (first entry)

XX 04-SEP-2000 (first entry)

XX Amino acid sequence of a human caspase-14.

XX Caspase-14; cell death specific protease; apoptosis stimulator;
XX apoptosis; AIDS; neurodegenerative disease; ischemic injury.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region /note= "large subunit"

XX Active-site 130..134

XX Cleavage-site 146..147

XX Region /note= "small subunit"

XX W0200028047-A1.

XX 18-MAY-2000.

XX 29-OCT-1999; 99WO-US025523.

XX 06-NOV-1998; 98US-00187789.

XX (UYE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES, Fernandez-Alnemri T;

XX WPI: 2000-376558/32.

XX N-PSDB: AAA15164.

XX Novel nucleic acids encoding cell death specific protease termed caspase-14 useful for treating cancers by stimulating apoptosis.

XX Claim 13; Fig 7; 78pp; English.

XX The present sequence represents a human caspase-14 polypeptide. The polypeptide is a cell death specific protease, and is an apoptosis stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase-14 antibodies are useful for treating or reducing the severity of pathological conditions associated with increased or decreased levels of

CC apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative
CC diseases and ischemic injury are treated by administering anti-caspase-14
CC antibodies. The antibody is useful for determining the presence or the
CC level of caspase-14 in tissue sample and also for the isolation of
CC caspase-14 with apoptotic activity or in screening assay to identify an
CC agent that inhibits heterodimer or heterotrimer formation and
CC therefore, apoptosis

XX Sequence 242 AA;

Query Match 99.6%; Score 1234; DB 3; Length 242;

Best Local Similarity 99.6%; Pred. No. 1.5e-120; Indels 0; Gaps 0;

Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPSLEEEKYDMSGALALILCVTKARSGSEEDLDLHMFRLRPESTMKDPTAEQ 60

Db 1 MSNPSLEEEKYDMSGARLALILCVTKARSGSEEDLDLHMFRLRPESTMKDPTAEQ 60

QY 61 FOELEKFOQALDSREDPVSCAFVYLMAGREGLKGDGMVKLENI.FEALNNKNCQAL 120

Db 61 FOELEKFOQALDSREDPVSCAFVYLMAGREGLKGDGMVKLENI.FEALNNKNCQAL 120

QY 121 RAKPKVYIIQACRGEQRPGETVGDEIVWYIKDSPQTIPTPTDNLHYSTVEGYIAYRH 180

Db 121 RAKPKVYIIQACRGEQRPGETVGDEIVWYIKDSPQTIPTPTDNLHYSTVEGYIAYRH 180

QY 181 DQKSCFIQTLVDVFTFRKGHIIELETVTRMAEALVDEGKARKTNPEIQTTLRKRLY 240

Db 181 DQKSCFIQTLVDVFTFRKGHIIELETVTRMAEALVDEGKARKTNPEIQTTLRKRLY 240

QY 241 LQ 242

Db 241 LQ 242

RESULT 2

AAG77980 ID AAG77980 standard; protein; 242 AA.

AC AAG77980;

DT 05-APR-2002 (first entry)

DE Full-length human caspase-14.

XX Human; caspase-14; anti-apoptotic; apoptosis.

XX Homo sapiens.

XX WO200181595-A2.

XX 01-NOV-2001.

XX 27-APR-2001; 2001WO-US013831.

XX 27-APR-2000; 2000US-0199962P.

XX (KNOL) KNOLL GMBH.

XX Mankovich JA;

XX WPI; 2002-041410/05.

XX N-PSDB; AAK98248.

XX Novel isolated human caspase-14 proteins and nucleic acid sequences,
XX useful for identifying modulators of caspase-14 protein that are useful
XX for modulating apoptosis.

XX Claim 20; Fig 1; 56p; English.

XX The sequence represents the novel full-length human caspase-14 protein,
XX referred to as "Caspase-14 NEW" in the specification. The invention
XX relates to a novel isolated human caspase-14 protein comprising an amino

CC acid sequence with MSNPSLE, at its amino terminus. The caspase-14 of
CC the invention has anti-apoptotic activity. Caspase-14 acts as a modulator
CC of caspase-14 activity. The polypeptide is useful for identifying a
CC compound which is a modulator of human caspase-14 activity, and is also
CC useful for identifying a compound which modulates the interaction of
CC caspase-14 with a target molecule. An antibody to caspase-14 is useful
CC for isolating the protein by standard techniques, and for detecting
CC caspase-14 to evaluate the abundance and expression pattern. The antibody
CC is also useful for diagnostically monitoring protein levels in a tissue
CC as a part of a clinical testing procedure. The polypeptide is useful as a
CC protease to cleave substrates and for inducing apoptosis in cells, in
CC screening assays, and as a bait protein in a two-hybrid or three-hybrid
CC assay to identify other proteins that interact with human caspase-14
CC protein

XX Sequence 242 AA;

Query Match 99.6%; Score 1234; DB 5; Length 242;

Best Local Similarity 99.6%; Pred. No. 1.5e-120; Indels 0; Gaps 0;

Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPSLEEEKYDMSGALALILCVTKARSGSEEDLDLHMFRLRPESTMKDPTAEQ 60

Db 1 MSNPSLEEEKYDMSGARLALILCVTKARSGSEEDLDLHMFRLRPESTMKDPTAEQ 60

QY 61 FOELEKFOQALDSREDPVSCAFVYLMAGREGLKGDGMVKLENI.FEALNNKNCQAL 120

Db 61 FOELEKFOQALDSREDPVSCAFVYLMAGREGLKGDGMVKLENI.FEALNNKNCQAL 120

QY 121 RAKPKVYIIQACRGEQRPGETVGDEIVWYIKDSPQTIPTPTDNLHYSTVEGYIAYRH 180

Db 121 RAKPKVYIIQACRGEQRPGETVGDEIVWYIKDSPQTIPTPTDNLHYSTVEGYIAYRH 180

QY 181 DQKSCFIQTLVDVFTFRKGHIIELETVTRMAEALVDEGKARKTNPEIQTTLRKRLY 240

Db 181 DQKSCFIQTLVDVFTFRKGHIIELETVTRMAEALVDEGKARKTNPEIQTTLRKRLY 240

QY 241 LQ 242

Db 241 LQ 242

RESULT 3

AAG77984 ID AAG77984 standard; protein; 242 AA.

AC AAG77984;

DT 05-APR-2002 (first entry)

DE Full-length human caspase-14 old.

XX Human; caspase-14; anti-apoptotic; apoptosis.

XX Homo sapiens.

XX WO200181595-A2.

XX 01-NOV-2001.

XX 27-APR-2001; 2001WO-US013831.

XX 27-APR-2000; 2000US-0199962P.

XX (KNOL) KNOLL GMBH.

XX Mankovich JA;

XX WPI; 2002-041410/05.

XX Novel isolated human caspase-14 proteins and nucleic acid sequences,
XX useful for identifying modulators of caspase-14 protein that are useful
XX for modulating apoptosis.

XX The sequence represents the novel full-length human caspase-14 protein,
XX referred to as "Caspase-14 NEW" in the specification. The invention
XX relates to a novel isolated human caspase-14 protein comprising an amino

XX Example; Fig 1; 58pp; English.

CC The sequence represents the full-length human caspase-14 protein,
 CC referred to as "caspase-14 OLP" in the specification. The invention
 CC relates to a novel isolated human caspase-14 protein comprising an amino
 CC acid sequence with MSNPSSLE, at its amino terminus. The caspase-14 of
 CC the invention has anti-apoptotic activity. Caspase-14 acts as a modulator
 CC of caspase-14 activity. The polypeptide is useful for identifying a
 CC compound which is a modulator of human caspase-14 activity, and is also
 CC useful for identifying a compound which modulates the interaction of
 CC caspase-14 with a target molecule. An antibody to caspase-14 is useful
 CC for isolating the protein by standard techniques, and for detecting
 CC caspase-14 to evaluate the abundance and expression pattern. The antibody
 CC is also useful for diagnostically monitoring protein levels in a tissue
 CC as a part of a clinical testing procedure. The polypeptide is useful as a
 CC protease to cleave substrates and for inducing apoptosis in cells, in
 CC screening assays, and as a bait protein in a two-hybrid or three-hybrid
 CC assay to identify other proteins that interact with human caspase-14
 CC protein.

CC Sequence 242 AA;

Query Match 96.0%; Score 1189; DB 5; Length 242;
 Best Local Similarity 99.6%; Pred. No. 7.6e-116;
 Matches 232; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 EKYDMSGALALILCTYKAREGSEEDLDALHMFRLQRFESTMKRDPPTAEQFQEELEKQ 69
 DB 10 EKYDMSGALALILCTYKAREGSEEDLDALHMFRLQRFESTMKRDPPTAEQFQEELEKQ 69
 QY 70 QAIIDSEDEPVSQAFVILMAHGRGFLKGEDEGVKLENTFEALNNKCCALRAKPKVYII 129
 DB 70 QAIIDSEDEPVSQAFVILMAHGRGFLKGEDEGVKLENTFEALNNKCCALRAKPKVYII 129
 QY 130 QACRGQRDPGETVGDDEIVMTIKDSPQITPTDYLHYVSTVEGYIAYRHQKSGCFIQ 189
 DB 130 QACRGQRDPGETVGDDEIVMTIKDSPQITPTDYLHYVSTVEGYIAYRHQKSGCFIQ 189
 QY 190 TLVDVETTKRGHILELITEVTRMAEAEIVQEGKARKINPEIOSTLRKRLYLQ 242
 DB 190 TLVDVETTKRGHILELITEVTRMAEAEIVQEGKARKINPEIOSTLRKRLYLQ 242

RESULT 4

AA68865
 ID AAY68865 standard; protein; 229 AA.

XX AAY68865;

DT 16-MAY-2000 (first entry)

DE Amino acid sequence of a human caspase-14 polypeptide.

XX Mouse; caspase-like polypeptide; human; caspase; apoptosis; skin disease;
 KW keratinisation; wound healing.

OS Homo sapiens.

PN WO200004169-A1.

PD 27-JAN-2000.

PF 12-JUL-1999; 99WO-EP004939.

PR 17-JUL-1998; 98EP-00202422.

PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

XX Van De Craen M, Declercq W, Vandenaabeele P, Fiers W;

XX WPI; 2000-182433/16.

DR N-PSDB; MAZ60684.

XX New murine and human caspase homologues useful for treating skin related
 PT disorders.

PS Claim 2; Page 53-54; 68pp; English.

CC The present sequence represents a human caspase-like polypeptide. The
 CC specification also describes a murine caspase-like polypeptide. Caspases
 CC are cysteinyl aspartate-specific proteinases which play a central role in
 CC apoptosis. The polypeptides of the invention are related to human and
 CC murine caspase-2 and human caspase-9, and possess all of the typical
 CC amino acids involved in catalysis, including the QACRG box, and contain
 CC no or only a very short prodomain. mRNA expression of the homologues of
 CC the invention is predominant in the skin. The caspase-like polypeptides
 CC are useful for treating human or animal diseases, such as skin diseases.
 CC They are also useful for screening for compounds that modulate its
 CC activity, i.e. agonists, antagonists, and inhibitors. The caspase-like
 CC polypeptides and polynucleotides are useful for modulating
 CC keratinisation, for diagnosing and treating inappropriate wound healing

CC Sequence 229 AA;

Query Match 94.1%; Score 1166; DB 3; Length 229;
 Best Local Similarity 99.6%; Pred. No. 1.8e-113;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 MCGALALILCTYKAREGSEEDLDALHMFRLQRFESTMKRDPPTAEQFQEELEKQ 73
 DB 1 MCGARLALILCTYKAREGSEEDLDALHMFRLQRFESTMKRDPPTAEQFQEELEKQ 60
 QY 74 SREDPVSQAFVILMAHGRGFLKGEDEGVKLENTFEALNNKCCALRAKPKVYIIQACR 133
 DB 61 SREDPVSQAFVILMAHGRGFLKGEDEGVKLENTFEALNNKCCALRAKPKVYIIQACR 120
 QY 134 GEQRDPGETVGDDEIVMTIKDSPQITPTDYLHYVSTVEGYIAYRHQKSGCFIQ 193
 DB 121 GEQRDPGETVGDDEIVMTIKDSPQITPTDYLHYVSTVEGYIAYRHQKSGCFIQ 180
 QY 194 VPTKRGHILELITEVTRMAEAEIVQEGKARKINPEIOSTLRKRLYLQ 242
 DB 181 VPTKRGHILELITEVTRMAEAEIVQEGKARKINPEIOSTLRKRLYLQ 229

RESULT 5

AA93216
 ID AAY93216 standard; protein; 214 AA.

XX AAY93216;

DT 04-SEP-2000 (first entry)

DE Amino acid sequence of a human caspase-14 splice variant.

XX Caspase-14; cell death specific protease; apoptosis stimulator;
 KW apoptosis; AIDS; neurodegenerative disease; ischemic injury.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Active-site 102..106

PN WO200028047-A1.

PD 18-MAY-2000.

PF 29-OCT-1999; 99WO-US025523.

PR 06-NOV-1998; 98US-00187789.

PA (UYE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES, Fernandez-Alnemri T;

DR WPI; 2000-376558/32.
DR N-PSDB; AAL1516.
XX
XX Novel nucleic acids encoding cell death specific protease termed caspase-14 useful for treating cancers by stimulating apoptosis.
PT
PT
XX
XX
PS Claim 42; Fig 9; 78pp; English.
XX
XX The present sequence represents a human caspase-14 splice variant. The
CC polypeptide is a cell death specific protease, and is an apoptosis
CC stimulator. Caspase-14, polynucleotides and polypeptides, and anti-caspase
CC -14 antibodies are useful for treating or reducing the severity of
CC pathological conditions associated with increased or decreased levels of
CC apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative
CC diseases and ischemic injury are treated by administering anti-caspase-14
CC antibodies. The antibody is useful for determining the presence of the
CC level of caspase-14 in tissue sample and also for the isolation of
CC caspase-14 with apoptotic activity or in screening assay to identify an
CC agent that inhibits heterodimer or heterotetramer formation and
CC therefore, apoptosis
XX
SQ Sequence 214 AA;

Query Match 86.0%; Score 1065; DB 3; Length 214;
Best Local Similarity 88.0%; Pred. No. 6.2e-103;
Matches 213; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MSNPRSLSEEEKYDMSGALMLILCVTKARSGSEEDLALHMFQRLPFESTMKRDPYAAQ 60
Db 1 MSNPRSLSEEEKYDMSGALMLILCVTKARSGSEEDLALHMFQRLPFESTMKRDPYAAQ 34
QY 61 FOELEKFOQAIDSRDPVSCAFVVLMAHGEGLKGEDEMYLLENLFEALNNKNCAL 120
Db 35 --BELKFPQALDSREDPVSCAFVVLMAHGEGLKGEDEMYLLENLFEALNNKNCAL 92
QY 121 RAKPKVYIIQACRGEQDPGRTVGGDEIVVYIKDSPQTIPTTYDHALHVSIVGCIYAYRH 180
Db 93 RAKPKVYIIQACRGEQDPGRTVGGDEIVVYIKDSPQTIPTTYDHALHVSIVGCIYAYRH 152
QY 181 DOKSGCFIQLTVDFYTRKGGHILELTVTRMAEALVQEGARKNPEIOSTRKELY 240
Db 153 DOKSGCFIQLTVDFYTRKGGHILELTVTRMAEALVQEGARKNPEIOSTRKELY 212
QY 241 LQ 242
Db 213 LQ 214

RESULT 6
AAY68864
ID AAY68864 standard; protein; 257 AA.
XX
AC AAY68864;
XX
DT 16-MAY-2000 (first entry)
XX
DE Amino acid sequence of a murine caspase-like polypeptide.
XX
KW Mouse; caspase-like polypeptide; human; caspase; apoptosis; skin disease;
XX keratinisation; wound healing.
XX
OS Mus musculus.
XX
XX
XX WO200004169-A1.
XX
PD 27-JAN-2000.
XX
XX
XX 12-JUL-1999; 99MO-EP004939.
XX
XX 17-JUL-1998; 98EP-0020422.
XX
XX
XX (VLAAS-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

PI Van De Craen M, Declercq W, Vandenaebale P, Fiers W;
XX
XX WPI; 2000-182433/16.
DR N-PSDB; AAZ60683.
XX
XX
XX
XX New murine and human caspase homologues useful for treating skin related disorders.
PS Claim 1; Page 51-52; 68pp; English.
XX
XX

XX The present sequence represents a murine caspase-like polypeptide. The
CC specification also describes a human caspase-like polypeptide. Caspases
CC are cysteine1 aspartate-specific proteinases which play a central role in
CC apoptosis. The polypeptides of the invention are related to human and
CC murine caspase-2 and human caspase-9, and possess all of the typical
CC amino acids involved in catalysis, including the QACRG box, and contain
CC no or only a very short prodomain. mRNA expression of the homologues of
CC the invention is predominant in the skin. The caspase-like polypeptides
CC are useful for treating human or animal diseases, such as skin diseases.
CC They are also useful for screening for compounds that modulate its
CC activity, i.e. agonists, antagonists, and inhibitors. The caspase-like
CC polypeptides and polynucleotides are useful for modulating
CC keratinisation, for diagnosing and treating inappropriate wound healing
XX
SQ Sequence 257 AA;

Query Match 75.4%; Score 934.5; DB 3; Length 257;
Best Local Similarity 70.9%; Pred. No. 3.8e-89;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;

QY 1 MSNPRSLSEEEKYDMSGALMLILCVTKARSGSEEDLALHMFQRLPFESTMKRDPYAAQ 60
Db 5 MSPQPLQEBRYDMSGRLALTLCTVKARSGSEEDMALHMFQRLPFESTMKRDPYAAQ 64
QY 61 FOELEKFOQAIDSRDPVSCAFVVLMAHGEGLKGEDEMYLLENLFEALNNKNCAL 120
Db 65 FLEELDFEQTINWEEPVSCAFVVLMAHGEGLKGEDEMYLLENLFEALNNKNCAL 124
QY 121 RAKPKVYIIQACRGEQDPG-----ETVGGDEIVVYIKDSPQTIPTTYDHALH 168
Db 125 RAKPKVYIIQACRGEQDPGELRGNEELGDELDGDE--VAVLKNNPQSIPTTYDHALH 183
QY 169 YSTVEGIYAVRHQKSGCFIQLTVDFYTRKGGHILELTVTRMAEALVQEGARKN 228
Db 184 YSTVEGIYAVRHQKSGCFIQLTVDFYTRKGGHILELTVTRMAEALVQEGARKN 243
QY 229 PEIOSTRKRLYDQ 242
Db 244 PEIOSTRKRLYDQ 257

RESULT 7
AAW93592
ID AAW93592 standard; protein; 281 AA.
XX
AC AAW93592;
XX
DT 21-JUN-1999 (first entry)
XX
DE Mouse caspase-14 protein.
XX
XX
XX Caspase-14; murine; protease; treatment; apoptotic-related disease;
XX autoimmune disease; cancer; acquired immunodeficiency syndrome; AIDS;
XX neurodegenerative disease; ischemic injury; anti-idiotypic antibody;
XX caspase-14 processing activity; epitope; competitor; modulator.
XX
XX Mus sp.
XX
XX WO9910504-A2.
XX
XX 04-MAR-1999.
XX
XX 26-AUG-1998; 98MO-US017715.
XX
XX
XX

Query Match	38.1%;	Score 472.5;	DB 5;	Length 234;
Best Local Similarity	45.0%;	Pred. No. 8.1e-41;		
Matches 107; Conservative	47;	Mismatches 73;	Indels 11;	Gaps 7

QY 11 KYDMSGALALILCVTKAREGSEEDLDALHMFRLQRFESTMKRDPFAEQFOELKRFQ 70
DB 1 CYDLSKAPALLLAVIQGRPGAHQHDVEALGGLCMALGFETTVRTPTAQAFQELHAFRE 60
QY 71 AIDSEEDPVSCAFVVLMAH-GRGFLKGEDGEMVXLENFALNNKNCQALRAKRYVII 129
DB 61 QLDTCRGVPSCHLVLMAGGPRGQLTGADGGEVQPEALMOELS--RCQVLQGRPKIFLL 118
QY 130 QACRGQRDPGETVSGDEIVWYIK--DSPQITPTDHALHYSTVEGYIAYRHQSGSCF 187
DB 119 QACRGGRNDAG--VGPTALPWYMSWLRAPPSVPSHADVLQIYAAQGYAVYR-DDKGSDF 175
QY 188 IQTLVDVFTKRGH-ILIELTEVTRMAEALVQ--GKARKTNPETIOSTLRRLYLQ 242
DB 176 IQTLVEVLRANPGRDLIELTEVNRKVCQEVILGPPCDELRAKCIETRSRLRLCQ 233

RESULT 11
ABG76499
ID ABG76499 standard; protein, 398 AA.
AC ABG76499;
XX
XX 05-NOV-2002 (first entry)
DE
XX
XX DNA encoding protein modification and maintenance molecule #3.
XX
XX Protein modification and maintenance molecule; gastrointestinal disorder;
XX dysphagia; esophageal spasm; gastritis; anorexia; nausea; hypertension;
XX cardiovascular disorder; atherosclerosis; vasculitis; aneurysm; allergy;
XX ischemic heart disease; autoimmune disorder; inflammatory disorder;
XX acquired immunodeficiency syndrome; AIDS; ankylosing spondylitis; cancer;
XX anaemia; amyloidosis; cell proliferative; arteriosclerotic bursts;
XX cirrhosis; developmental disorder; renal tubular acidosis; anaemia;
XX bone resorption; epilepsy; epithelial disorder; keratosis pilaris;
XX allergic contact dermatitis; insect bite; keloid; dermatofibroma; eczema;
XX neurological disorder; stroke; cerebral neoplasm; Alzheimer's disease;
XX Huntington's disease; dementia; reproductive disorder; infertility;
XX endometriosis; gynecomastia; ectopic pregnancy; gene therapy.
XX
XX Homo sapiens.
XX
XX WO200260942-A2.
XX
XX 08-AUG-2002.
XX
XX 30-JAN-2002; 2002WO-US002813.
XX
XX 31-JAN-2001; 2001US-0265705P.
XX 05-FEB-2001; 2001US-0266762P.
XX 16-FEB-2001; 2001US-0269581P.
XX 23-FEB-2001; 2001US-0271198P.
XX 01-MAR-2001; 2001US-0272813P.
XX 13-MAR-2001; 2001US-0275566P.
XX 23-MAR-2001; 2001US-0278505P.
XX 30-MAR-2001; 2001US-0280539P.
XX
XX (INCYTE GENOMICS INC.
XX
XX Warren BA, Honchell CD, Lu Y, Walia NK, Burford N, Delegeane AM;
XX Gaudin AR, Baughn MR, Griffin JA, Gietzen KJ, Lu DM, Ison CH;
XX Rankumar J, Tang TY, Lal PG, Borowski ML, Duggan BM, Hafalia AJA;
XX Ariznu C, Thangaveilu K, Yao MG, Elliott VS, Ding L, Yue H, Lee S;
XX Swarnakar A, Tien UK, Xu Y;
XX
XX WPI, 2002-608499/65.
XX
XX N-PSDB; ABS58370.
XX
XX
XX New protein modification and maintenance molecules useful for treating or
XX preventing gastrointestinal, cardiovascular, autoimmune/inflammatory,
XX cell proliferative, developmental, neurological and reproductive
XX disorders.

PS Claim 1; Page 133-134; 172pp; English.
XX
XX The invention describes an isolated human polypeptide (I), a naturally
XX occurring amino acid sequence at least 90 % identical to the protein, or
XX a biologically active fragment or an immunogenic fragment of the protein.
XX The protein modification and maintenance molecules are useful in the
XX diagnosis, treatment, and prevention of gastrointestinal (e.g. dysphagia,
XX esophageal spasm, gastritis, anorexia or nausea), cardiovascular (e.g.
XX atherosclerosis, hypertension, vasculitis, aneurysm, or ischemic heart
XX disease), autoimmune/inflammatory (e.g. acquired immunodeficiency
XX syndrome (AIDS), allergies, ankylosing spondylitis, anaemia or
XX amyloidosis), cell proliferative (e.g. cancers, arteriosclerotic,
XX bursts, or cirrhosis), developmental (e.g. renal tubular acidosis,
XX anaemia, bone resorption, or epilepsy), epithelial (e.g. allergic contact
XX dermatitis, keratosis pilaris, insect bites, keloid, dermatofibroma or
XX eczema), neurological (e.g. stroke, cerebral neoplasms, Alzheimer's
XX disease, Huntington's disease or dementia), and reproductive disorders
XX (e.g. infertility, endometriosis, gynecomastia or ectopic pregnancy).
XX These may also be used in assessing the effects of exogenous compounds on
XX the expression of nucleic acid and amino acid sequences of protein
XX modification and maintenance molecules. Polynucleotides are useful in
XX somatic and germline gene therapy. This is the amino acid sequence of a
XX protein modification and maintenance molecule described in the invention
XX
XX Sequence 398 AA:
XX
XX Query Match 38.1%; Score 472.5; DB 5; Length 398;
XX Best Local Similarity 45.0%; Pred. No. 1.7e-40;
XX Matches 107; Conservative 47; Mismatches 73; Indels 11; Gaps 7;
XX
QY 11 KYDMSGALALILCVTKAREGSEEDLDALHMFRLQRFESTMKRDPFAEQFOELKRFQ 70
DB 165 QYDLSKAPALLLAVIQGRPGAHQHDVEALGGLCMALGFETTVRTPTAQAFQELHAFRE 224
QY 71 AIDSEEDPVSCAFVVLMAH-GRGFLKGEDGEMVXLENFALNNKNCQALRAKRYVII 129
DB 225 QLDTCRGVPSCHLVLMAGGPRGQLTGADGGEVQPEALMOELS--RCQVLQGRPKIFLL 282
QY 130 QACRGQRDPGETVSGDEIVWYIK--DSPQITPTDHALHYSTVEGYIAYRHQSGSCF 187
DB 283 QACRGGRNDAG--VGPTALPWYMSWLRAPPSVPSHADVLQIYAAQGYAVYR-DDKGSDF 339
QY 188 IQTLVDVFTKRGH-ILIELTEVTRMAEALVQ--GKARKTNPETIOSTLRRLYLQ 242
DB 340 IQTLVEVLRANPGRDLIELTEVNRKVCQEVILGPPCDELRAKCIETRSRLRLCQ 397

RESULT 12
ABBI0110
ID ABBI0110 standard; protein, 452 AA.
XX
XX ABBI0110;
XX
XX 26-JUL-2002 (first entry)
XX
XX Mouse caspase 2 protein.
XX
XX Caspase 2; antiapoptotic; cytoskeletal; osteopathic; cerebroprotective;
XX neuroprotective; antilipemic; antiinflammatory; antitubercular;
XX haematopoietic disorder; bone metabolism disorder; cholesteral disorder;
XX hyperproliferative disorder; cancer; blood disorder; stroke;
XX brain injury; neurodegenerative disease; infection; inflammation; tumour.
XX
XX Mus musculus.
XX
XX WO200224720-A1.
XX
XX 28-MAR-2002.
XX
XX 14-SEP-2001; 2001WO-US028631.
XX
XX 20-SEP-2000; 2000US-00667018.
XX

PA (ISIS-) ISIS PHARM INC.
 XX Zhang H, Walt AT;
 XX
 DR WPI; 2002-351998/38.
 XX N-PSDB; ABB58563.
 XX
 PT New antisense compounds targeted to nucleic acid molecule encoding
 PT caspase 2, useful for treating diseases or conditions associated with
 PT caspase 2, e.g. cancer, blood disorders, stroke, brain injury and
 PT neurodegenerative diseases.
 PS Example 13; Page 111-113; 146pp; English.
 XX
 CC The invention relates to a compound 8-50 nucleobases in length targeted
 CC to a nucleic acid molecule encoding caspase 2, which specifically
 CC hybridizes with and inhibits the expression of caspase 2, or specifically
 CC hybridizes with at least an 8-nucleobase portion of an active site on a
 CC nucleic acid molecule encoding caspase 2. The activity of antisense
 CC oligonucleotides of the invention may be described as, cytostatic,
 CC osteoprotective, cerebroprotective, neuroprotective, antilipemic,
 CC antiinflammatory and antimicrobial. The antisense compounds are useful
 CC for treating an animal having a disease or condition associated with
 CC caspase 2, such as hematopoietic disorder, bone metabolism disorder,
 CC cholesterol disorder, or a hyperproliferative disorder. These compounds
 CC may further be used as research reagents and diagnostics, to distinguish
 CC between functions of various members of a biological pathway, in the
 CC treatment of a disease or disorder which can be treated by modulating the
 CC expression of caspase 2, including cancer, blood disorders, stroke, brain
 CC injury and neurodegenerative diseases. They may also be used for
 CC prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
 CC formation. The current sequence represents the mouse caspase 2 protein
 XX
 SQ Sequence 452 AA;
 Query Match 23.8%; Score 295; DB 5; Length 452;
 Best Local Similarity 31.5%; Pred. No. 8.2e-22;
 Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;
 QY 29 REGSEBDLALHEMFROLRFESTMKRDPFAEQFOELEKEFOAIDSREDPVSCAFVYMA 88
 Db 219 RSGGDVDTTLVTLFKLIGNVAVLHDQTAQEMQKLNPAQ-LPARVTDSCV-VALLS 276
 QY 89 HGEGBFLKEDGEMVYKLENI.FEALNNKNCQALAKRKYVYIIQACRGQRDPG----- 140
 Db 277 HGEVGGIYGVDSKLDLQLEVFRLFDNANCPSLQNKPKMFPFIQACRGDETDRGVDDQDGN 336
 QY 141 -----ETVGGDEIVMYIKDSPQITPTTDALHYSTVEGYIAYRHQDGSCTIQTIV 192
 Db 337 HTQSPCESDPAKKEELMKR-----LPTKSDMICGACIKGNAAAMNTKSGSWYTEALT 391
 QY 193 DVFTK-KGHITELLTEVTRMAEALVQEGKARKTN-----PEIGSTLRKRLYL 241
 Db 392 QVFSERACDMHVDMLVKYNALIKE-----REGVAPGTEFHRCKEMGEYSCTLCOQLYL 445
 RESULT 13
 ADB79812
 ID ADB79812 standard; protein; 452 AA.
 XX
 AC ADB79812;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Rat caspase 2, Ich-1, SEQ ID 52.
 XX
 KW Analgesic; pain; streptozocin-induced diabetes; rat.
 XX
 OS Rattus norvegicus.
 XX
 PN EPI279744-A2.
 XX
 PD 29-JAN-2003.

XX
 PF 26-JUL-2002; 2002EP-00255249.
 XX
 PR 27-JUL-2001; 2001GB-00018354.
 XX
 PR 07-FEB-2002; 2002GB-00002910.
 XX
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Brooksbark RA, Dixon AK, Lee K, Pinnock RD;
 XX
 DR WPI; 2003-395407/38.
 XX N-PSDB; ADB79813.
 XX
 PT Use of isolated gene sequences and encoded polypeptides that are
 PT upregulated in the spinal cord in response to streptozocin-induced
 PT diabetes for screening compounds for the treatment of pain, or for
 PT diagnosing pain.
 XX
 PS Claim 1; Page 115-117; 334pp; English.
 CC The present invention relates to nucleotide sequences which are useful in
 CC the screening of compounds for the treatment of pain, or for the
 CC diagnosis of pain. The nucleotide sequences are up-regulated in the
 CC spinal cord in response to streptozocin-induced diabetes. The present
 CC sequence was used to illustrate the invention.
 XX
 SQ Sequence 452 AA;
 Query Match 23.6%; Score 293; DB 7; Length 452;
 Best Local Similarity 31.5%; Pred. No. 1.3e-21;
 Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;
 QY 29 REGSEBDLALHEMFROLRFESTMKRDPFAEQFOELEKEFOAIDSREDPVSCAFVYMA 88
 Db 219 RSGGDVDTTLVTLFKLIGNVAVLHDQTAQEMQKLNPAQ-LPARVTDSC-IVALLS 276
 QY 89 HGEGBFLKEDGEMVYKLENI.FEALNNKNCQALAKRKYVYIIQACRGQRDPG----- 140
 Db 277 HGEVGGIYGVDSKLDLQLEVFRLFDNANCPSLQNKPKMFPFIQACRGDETDRGVDDQDGN 336
 QY 141 -----ETVGGDEIVMYIKDSPQITPTTDALHYSTVEGYIAYRHQDGSCTIQTIV 192
 Db 337 HAQSPCESDPAKKEELMKR-----LPTKSDMICGACIKGNAAAMNTKSGSWYTEALT 391
 QY 193 DVFTK-KGHITELLTEVTRMAEALVQEGKARKTN-----PEIGSTLRKRLYL 241
 Db 392 QVFSERACDMHVDMLVKYNALIKE-----REGVAPGTEFHRCKEMGEYSCTLCOQLYL 445
 RESULT 14
 ADE63000
 ID ADE63000 standard; protein; 452 AA.
 XX
 AC ADE63000;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Rat Protein AAB96379, SEQ ID NO 8934.
 XX
 KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX
 OS Rattus norvegicus.
 XX
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002MO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 XX
 PR 01-NOV-2001; 2001US-0346382P.
 XX
 PR 26-NOV-2001; 2001US-0333347P.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:43:31 ; Search time 49.5 Seconds
(without alignments)
1542.533 Million cell updates/sec

Title: US-10-068-564-5

Perfect score: 1239
Sequence: 1 MSNPSLEEEKYDMSCALAA.....KARKTNPETQSTLRKRLYLQ 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_RHCHL_25:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mmc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_virus:*
17: sp_bacteriophage:*
17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	298	24.1	452	11	Q8C9H7 mus musculus
2	295	23.8	452	11	Q8K241 mus musculus
3	293	23.6	452	11	O55194 rat mus musculus
4	289.5	23.4	423	13	Q91B67 xenopus lae
5	289	23.3	435	4	Q9BUP7 homo sapien
6	284.5	23.0	283	13	Q93417 gallus gall
7	279.5	22.6	316	5	Q817B0 geodia cydo
8	279.5	22.6	426	5	O81672 geodia cydo
9	275.5	22.2	277	6	O8MUT3 oryctolagus
10	275.5	22.2	277	6	O8MUT1 felis silve
11	274.5	22.2	277	6	Q95ND5 sus scrofa
12	274.5	22.2	383	13	Q91917 brachydano
13	273.5	22.1	313	11	Q8CHV5 mus musculus
14	272.5	22.0	277	6	O8MK15 canis famli
15	272	22.0	399	13	Q91B63 xenopus lae
16	270	21.8	303	11	O88550 rat mus musculus

17	269.5	21.8	452	11	Q9R0T0 mus musculus
18	269	21.7	482	13	Q90WT1 gallus gall
19	266.5	21.5	282	13	Q98U18 brachydano
20	264.5	21.3	290	13	O81S8 oryzae lat
21	263.5	21.3	453	11	O8C300 mus musculus
22	263.5	21.3	454	11	O8C309 mus musculus
23	261.5	21.1	289	5	Q86F10 anopheles s
24	260.5	21.0	403	13	Q90WU0 gallus gall
25	257	20.7	476	13	Q91B73 brachydano
26	256	20.7	500	13	Q91B64 xenopus lae
27	256	20.7	520	13	Q91B62 xenopus lae
28	255	20.6	417	5	Q9YIU6 pristinonchu
29	254.5	20.5	454	11	Q9JHK1 ractus norv
30	250.5	20.2	380	13	Q80W99 fuqua rubrip
31	250.5	20.2	318	13	Q91B65 xenopus lae
32	249.5	20.1	280	13	O81G42 fuqua rubrip
33	248	20.0	522	4	O81UP5 homo sapien
34	242.5	19.6	189	11	O8BNT4 mus musculus
35	242.5	19.6	276	11	Q9D089 mus musculus
36	242.5	19.6	280	13	O81S9 oryzae lat
37	241.5	19.5	276	11	Q99M47 mus musculus
38	239.5	19.3	293	5	O819V7 bombyx mori
39	236.5	19.1	299	5	O81955 spodoptera
40	235.5	19.0	182	6	O77623 ovis aries
41	235	19.0	277	11	O35397 ractus norv
42	232.5	18.8	328	5	O81TP3 brachydano
43	230.5	18.6	482	11	Q9JHX4 ractus norv
44	228.5	18.4	347	5	Q9GVB9 hydra atten
45	228.5	18.4	404	13	Q9DDJ2 brachydano

ALIGNMENTS

RESULT 1
ID Q8C9H7 PRELIMINARY; PRT; 452 AA.
AC Q8C9H7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 2.
GN CASP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
ON NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=2354683; PubMed=1246851;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK042072; BAC31153.1; -
DR MGD; MGI:97295; Casp2.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PRO0376; ILIBENZYMZ.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.

DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 452 AA; 50689 MW; C3715908508619CA CRC64;

Query Match 24.1%; Score 298; DB 11; Length 452;
Best Local Similarity 31.9%; Pred. No. 5.8e-17;
Matches 76; Conservative 51; Mismatches 75; Indels 36; Gaps 7;

QY 29 RSGSDVHTTLVTLFKLIGVNVHLHDQTAQEMQKQNFQAQ-LPAHRYTDSCV-VALLS 276
DB 219 RSGSDVHTTLVTLFKLIGVNVHLHDQTAQEMQKQNFQAQ-LPAHRYTDSCV-VALLS 276
QY 89 HGRGFLKGEDEGVNKLIENTFEALNNKNCOALRAKPKVYIIQAQCRGORDPG----- 140
DB 277 HGVGGIYGVGDKLLQQLQEVFRLFDNMNCPSLQNKPKPMFFIQAQCRGETRGVDQDGKN 336
QY 141 -----ETVGGDEIVMWIKDSPQITPTTDALHVSIVYEGYIAYRHDKGSCFIQTLLV 192
DB 337 HTQSPGCEESDAGKEELMKR-----LPTRSDMTCGYACLKGNAMNTRKGSWYIALT 391
QY 193 DVFTKR--KSHILELLETVTRMAEALVQEGKARKTN-----PEIQTTRKRYL 241
DB 392 QVFSERACDWHVADMVKNVALLKE---REGYAPGTEHFRCKEMSEYCSITLCOQLYL 445

RESULT 2

Q8K241 PRELIMINARY; PRT; 452 AA.
AC Q8K241;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-2.
GN CASP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RA Strassberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034262; AAH34262.1; -.
DR MGI; MGI:97295; Casp2.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCNZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 452 AA; 50661 MW; A4DE25A712PAB855 CRC64;

Query Match 23.8%; Score 295; DB 11; Length 452;
Best Local Similarity 31.5%; Pred. No. 1e-16;
Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

QY 29 RSGSDVHTTLVTLFKLIGVNVHLHDQTAQEMQKQNFQAQ-LPAHRYTDSCV-VALLS 276
DB 219 RSGSDVHTTLVTLFKLIGVNVHLHDQTAQEMQKQNFQAQ-LPAHRYTDSCV-VALLS 276
QY 89 HGRGFLKGEDEGVNKLIENTFEALNNKNCOALRAKPKVYIIQAQCRGORDPG----- 140

DB 219 RSGSDVHTTLVTLFKLIGVNVHLHDQTAQEMQKQNFQAQ-LPAHRYTDSCV-VALLS 276
QY 89 HGRGFLKGEDEGVNKLIENTFEALNNKNCOALRAKPKVYIIQAQCRGORDPG----- 140
DB 277 HGVGGIYGVGDKLLQQLQEVFRLFDNMNCPSLQNKPKPMFFIQAQCRGETRGVDQDGKN 336
QY 141 -----ETVGGDEIVMWIKDSPQITPTTDALHVSIVYEGYIAYRHDKGSCFIQTLLV 192
DB 337 HTQSPGCEESDAGKEELMKR-----LPTRSDMTCGYACLKGNAMNTRKGSWYIALT 391
QY 193 DVFTKR--KSHILELLETVTRMAEALVQEGKARKTN-----PEIQTTRKRYL 241
DB 392 QVFSERACDWHVADMVKNVALLKE---REGYAPGTEHFRCKEMSEYCSITLCOQLYL 445

RESULT 3

Q05194 PRELIMINARY; PRT; 452 AA.
AC Q05194;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NEDD2/ICH-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN NCBI_TaxID=10116;
RP SEQUENCE FROM N.A.
RA MEDLINE=98087427; PubMed=9427555;
RA Sato N., Milligan C.E., Uchiyama Y., Oppenheim R.W.;
RT "Cloning and expression of the cDNA encoding rat caspase-2.";
RL Gene 202:127-132 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SEPRAGUE-DAMLEY; TISSUE=Brain;
RA Jin K.L., Simon R.P., Graham S.H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; U77933; AAB96379.1; -.
DR EMBL; AF136231; AAD33684.1; -.
DR PIR; JC6507; UC6507.
DR HSP; P29466; 1ICE.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCNZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 452 AA; 50728 MW; 03F9D096BB741CE3 CRC64;

Query Match 23.6%; Score 293; DB 11; Length 452;
Best Local Similarity 31.5%; Pred. No. 1.5e-16;
Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

QY 29 RSGSDVHTTLVTLFKLIGVNVHLHDQTAQEMQKQNFQAQ-LPAHRYTDSCV-VALLS 276
DB 219 RSGSDVHTTLVTLFKLIGVNVHLHDQTAQEMQKQNFQAQ-LPAHRYTDSCV-VALLS 276
QY 89 HGRGFLKGEDEGVNKLIENTFEALNNKNCOALRAKPKVYIIQAQCRGORDPG----- 140

Db 277 HGVGGITVVDGKLTOLQEVFRIFDNANCPSLONKRFPIQACRGDETDRGVDOQDGN 336
QY 141 -----ETVSGDEIWMYIKDSPQITPTTADLHYSTVEGYIARHDQKSCFIQTLV 192
Db 337 HMQSPGCESDPAKKEMLMKR-----LPIRSDMICGYACIKGNAAARNTKRGSWYIEALT 391
QY 193 DVFTKR--KGIILELITETVRMAEALVQEGAKRTN-----PEIOSTLKRILYL 241
Db 392 QVFSERACDMHVMADMVKVNAALIKE---REGYAPCTEFRCKEMSEYCSITLCOQLYL 445

RESULT 4
Q91B67 PRELIMINARY; PRT; 423 AA.
ID Q91B67
AC Q91B67
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Caspase-2.
GN XCASPASE-2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yaotani Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
family";
RT J. Biol. Chem. 275:10484-10491 (2000).
DR EMBL; AB038168; BAA94746.1; -.
DR HSSP; P29466; 1ICE.
DR MEROPS; C14_006; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBENZIME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 423 AA; 47123 MW; E91EB1FD133F01FD CRC64;

Query Match 23.4%; Score 289.5; DB 13; Length 423;
Best Local Similarity 30.5%; Pred. No. 2.8e-16;
Matches 74; Conservative 51; Mismatches 71; Indels 47; Gaps 7;

QY 29 RSGSEEDLALHMFROLREFTMKRDPYABQFOEIEKFR-----QQAISREDPVSCAF 83
Db 187 RCGGEVVLASLEKLFSSIGYQVDRCNINAQSWMSQLGAFSAIPVHSALDS-----CV 239
QY 84 VVIMAHGRBEGFLGDEGMVKTLELFEALNNKNGCALRAKPKVYIITQACRGEDRPD--- 140
Db 240 VALLSHLDGAVGTGDKLVQLQEVFTALDNHCPQLQNKPKMFFIQCAGSEETDRGVQ 299
QY 141 -----ETVSGDEIWMYIKDSPQITPTTADLHYSTVEGYIARHDQKSCF 187
Db 300 RDRREGSGSPGCEGSDAGREDIKV-----RLPFGQSMTCAYACIKGTVSLRNTKRSWF 353
QY 188 IQTLVDVFTK--RKGHILELITETVRMAEALVQEGAKRTN-----PEIOSTLKR 238

Db 354 VQDLVSVRSQSKDTHVADMVKVNAALIKE-----REGYAPCTEFRCKEMSEYCSITLCKD 409
QY 239 IYL 241
Db 410 IYL 412

RESULT 5
Q9BUP7 PRELIMINARY; PRT; 435 AA.
ID Q9BUP7
AC Q9BUP7
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Similar to caspase 2 (Neural cell expressed, developmentally down-regulated 2).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Straussberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kalinine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koudina M., Raphael J., Moreira D., Kelley T., Lahaer J., Lin X.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDS in BD Creator (TM) System Donor
vector";
RT Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC002427; AAH02427.1; -.
DR EMBL; BT007240; AAP35904.1; -.
DR HSSP; P29466; 1ICE.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBENZIME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 435 AA; 48869 MW; 10CFA5A1F9369E57 CRC64;

Query Match 23.3%; Score 289; DB 4; Length 435;
Best Local Similarity 31.1%; Pred. No. 3.2e-16;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

QY 29 RSGSEEDLALHMFROLREFTMKRDPYABQFOEIEKFRQQAISREDPVSCAFVLLMA 88
Db 202 RSGGDVHDSTLVTLFKLGIDVAVLQDQTAQENQKQNTAQLPRAKRVYDSC-IYALLS 259
QY 89 HGRBEGFLGDEGMVKTLELFEALNNKNGCALRAKPKVYIITQACRGEDRPD--- 140
Db 260 HGVGALIVGDGKLTOLQEVFOLEFANANCPSLONKRFPIQACRGDETDRGVDOQDGN 319
QY 141 -----ETVSGDEIWMYIKDSPQITPTTADLHYSTVEGYIARHDQKSCFIQTLV 192

Db 320 HAGSGCESDAGE-----KLPKMRUPTRSDMTCGATACKGTAMNTRKSGYITIALA 374
 QY 193 DVFKR--KHGHELETVTRRMAEAEVQGRKRTN-----PEIQSTRRLY 241
 Db 375 QVFSEACDMHVALDVKVVALIND---REGVAPGTEFRCKEMSEVCSYTLCHRLYL 428

RESULT 6

093417 PRELIMINARY; PRT; 283 AA.
 ID 093417
 AC 093417
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Caspase-3
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20149872; PubMed=10684799;
 RA Johnson A.L., Bridgman J.T.;
 RT "Caspase-3 and -6 expression and enzyme activity in hen granulosa
 cells.";
 RL Biol. Reprod. 62:589-598(2000).
 DR EMBL: AF083029; AAC32602.1; -.
 DR HSSP: P42574; 1PAU.
 DR MEROPS: C14.003; -.
 DR GO: GO:0030693; F:caspase activity; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR002138; ICE_P10.
 DR InterPro: IPR001309; ICE_P20.
 DR InterPro: IPR002398; Peptidase_C14.
 DR Pfam: PF00656; Peptidase_C14.1.
 DR PRINTS: PR00376; ILBCEZYME.
 DR SMART: SM00115; CASC.1.
 DR PROSITE: PS01122; CASPASE_CYS.1.
 DR PROSITE: PS01121; CASPASE_HIS.1.
 DR PROSITE: PS50207; CASPASE_P10.1.
 DR PROSITE: PS50208; CASPASE_P20.1.
 DR SEQUENCE 283 AA; 31675 MW; 161242DDEFD4C4F CRC64;

Query Match 23.0%; Score 284.5; DB 13; Length 283;
 Best Local Similarity 30.3%; Pred. NO. 4.6e-16;
 Matches 76; Conservative 47; Mismatches 101; Indels 27; Gaps 7;

QY 7 IEERKYMGSALALILCVT-----KAREGSEEDLALHMRPQRFESTMKRDP 56
 Db 40 LPDDYRMDPELGVCTIINNKNFHDGTGLSSSGTDADAASREVMKLGKYKLANDL 99
 QY 57 TAEQOELEKFPQALDSREDPVSCAFVIMAHGREGFLGDEGEMVKTLENLFEALNNKN 116
 Db 100 SSMDIFKLKNVSEEDHSKRSFVC---VLISHGDEGLFYGTGDL-ELKVLNLSFRGDK 155
 QY 117 COALRAKPKYIIQACRGEORDPG--ETVGGDEILWVWIKSPQTIPTVDALHYGVESG 174
 Db 156 CRSLAKGKFFIQAQCGTELDGTEADSPDPTVC-----KRIPEADFLVAYSTAPG 209
 QY 175 YIAYRHDKQSCPIQTLVDVFTK--RKGHILELTVTRMAAEVY---QESKARKTNP 229
 Db 210 YYSWRNAEGSWFIQSLCRNLKEHARKLELMQILTVNRRVAVYEGSGTQDINAKKQID 269
 QY 230 EIQSTIKRLY 240
 Db 270 CIVSMILTKEY 280

RESULT 7
 0817B0 PRELIMINARY; PRT; 316 AA.
 ID 0817B0

AC 0817B0;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Caspase 3
 OS Geodia cydonium (Sponge).
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
 OC Astrophorida; Geodiidae; Geodia.
 OC NCBI_TaxID=6047;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wiens M., Saenger H., Krasko A., Perovic S., Mueller W.E.G.;
 RT "Caspase-mediated apoptosis in sponges: Cloning and function.";
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AJ417903; CAD10676.1; -.
 DR GO: GO:0030693; F:caspase activity; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR002138; ICE_P10.
 DR InterPro: IPR001309; ICE_P20.
 DR Pfam: PF00656; Peptidase_C14.1.
 DR PRINTS: PR00376; ILBCEZYME.
 DR SMART: SM00115; CASC.1.
 DR PROSITE: PS01122; CASPASE_CYS.1.
 DR PROSITE: PS01121; CASPASE_HIS.1.
 DR PROSITE: PS50207; CASPASE_P10.1.
 DR PROSITE: PS50208; CASPASE_P20.1.
 DR SEQUENCE 316 AA; 35319 MW; 33A46BCCE6C3F9B7 CRC64;

Query Match 22.6%; Score 279.5; DB 5; Length 316;
 Best Local Similarity 28.2%; Pred. No. 1.4e-15;
 Matches 78; Conservative 54; Mismatches 94; Indels 51; Gaps 9;

QY 9 EEKYDMSG--ALALIL-----CVTKAREGSEEDLALHMRPQRFESTMKRDPYAEQ 60
 Db 37 KDAYKMSRRPGRMALIINNKNFTCGMKERYGTDKDAENLYGLFNWLGMATIRKDNLTGKA 96
 QY 61 FQZLEKFPQALDSREDPVSCAFVIMAHGREGFLGDEGEMVKTLENLFEALNNKNCOAL 120
 Db 97 MTRFEEDLARDHSAVD---CVVVALILHGISGLYSTDGDLLPVBDLTCKYFGVNPSTL 153
 QY 121 RAKPKYIIQACRGEORDPG--ETVGG-----DEIVWVTKDSPOT- 158
 Db 154 IGKPKYFVYQACGKGFYVSESESDGBESYNNKETANEMKQDPKIVKALDADETD 213
 QY 159 -----IPTVDALHYSTVEGYIAYRHDKQSCPIQTLVDVFTKRGHILELLE 208
 Db 214 GGGYSREALPTEADFLVAVATVPGYVSWRNSGWFIKAFVDTMRDLASKHFMIDLTE 273
 QY 209 YTRRMAEAEVQGRKRTNPEIQ---STLRKRLYIQ 242
 Db 274 VNRKVA-----YDFOSRGRKQIPAPVTMLTRKLYER 305

RESULT 8

0816Y2 PRELIMINARY; PRT; 426 AA.
 ID 0816Y2
 AC 0816Y2
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Caspase-3.
 GN Geodia cydonium (sponge).
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
 OC Astrophorida; Geodiidae; Geodia.
 OC NCBI_TaxID=6047;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Eukaryota;
 RA Wiens M., Saenger H., Krasko A., Perovic S., Mueller W.E.G.;
 RT "Caspase-mediated apoptosis in sponges: cloning and function.";
 RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.


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Db      94 BOIYALDVSAREHSHKRSFFIC--VLLSHGEGIIYGTNGP-VDLKKLTGPFPGDYCR 149
QY      119 ALRAKPKYVITIOACRGEGRDPG-ETVGG--DEIMVNIKDSQOTIPYTDALHVVSTYEGY 175
Db      150 SLTGKPKFIIOACRGEGFLDGLIDSTEDDILAC-----OKIPEVADFLYAYSTAPGY 203
QY      176 IAYBHDKGSCFIOTLVDPFTKRKHILE--LITEVTRMA-EAEIVQEGKA--RKTN 228
Db      204 YSMRNSKDGSWFIQSLCSML-RLVAHLEFEMHILTRVNRKATFEFSISLDSALHGKKOI 262
QY      229 PEIQTSTARKRY 240
Db      263 PCIVSMLTKEYL 274

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RESULT 11

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ID      095ND5      PRELIMINARY;      PRT;      277 AA.
AC      095ND5;
DT      01-DEC-2001 (Tremblrel. 19, Created)
DT      01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE      01-OCT-2003 (Tremblrel. 25, Last annotation update)
OS      Caspase-3.
OC      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX      NCBI_Taxid=9823;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21334413; PubMed=11440638;
RA      Muneta Y., Shimojima Y., Mori Y.;
RT      "Porcine caspase-3: cloning and its activity during apoptosis of
RT      porcine PK15 cells induced by porcine Fas-ligand.";
RL      J. Interferon Cytokine Res. 21:409-415(2001).
DR      EMBL; AB029345; BAB55544.1; -.
DR      MEROB; C14.003; -.
DR      GO; GO:0030693; F:caspase activity; IEA.
DR      GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR      InterPro; IPR002138; ICE p10.
DR      InterPro; IPR001309; ICE p20.
DR      InterPro; IPR002398; Peptidase_C14.
DR      Pfam; PF00656; Peptidase_C14; 1.
DR      PRINTS; PR00376; IL1BCENZME.
DR      SMART; SM00115; CASc; 1.
DR      PROSITE; PS01122; CASPASE_CYS; 1.
DR      PROSITE; PS01121; CASPASE_HIS; 1.
DR      PROSITE; PS50207; CASPASE_P10; 1.
DR      PROSITE; PS50208; CASPASE_P20; 1.
SQ      SEQUENCE 277 AA; 31379 MW; 616C0F56141B012B CRC64;

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Query Match 22.2%; Score 274.5; DB 6; Length 277;

Best Local Similarity 37.3%; Pred. No. 3, 1e-15; Matches 82; Conservative 21; Mismatches 94; Indels 17; Gaps 8;

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QY      29 RSGSEEDLALHMFQRLRFSTMKRDPYAEQOELEKFAQALDSREDPVSCAFVYMA 88
Db      64 RSGTDVDAANILRTFNLKTEVANKDULTRERILELMSHVSKEHDHRSFFIC--VLLS 120
QY      89 HGESEGFLKGGDEGMVLENTLFEALNNKCOALRAKPKYVITIOACRGEGRDPG-ETVGGDE 147
Db      121 HGESEGFLKGGDEGMVLENTLFEALNNKCOALRAKPKYVITIOACRGEGRDPG-ETVGGDE 179
QY      148 IYVWIKDSQOTIPYTDALHVVSTYEGYIAYRHDKGSCFIOTLVDPFTKRKHILE-- 205
Db      180 DDMAC-----OKIPEVADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAL-KQYVHKLLEWH 234
QY      206 -LITEVTRMA-EAEIVQEGK--ARKTNPEIQTSTARKRY 240
Db      235 ILTRVNRKVAVEFESFSTDTSTFAKKQIPICTIVSMLTKEYL 274

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RESULT 12

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Q919L7
ID      0919L7      PRELIMINARY;      PRT;      383 AA.
AC      0919L7;
DT      01-OCT-2000 (Tremblrel. 15, Created)
DT      01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE      01-OCT-2003 (Tremblrel. 25, Last annotation update)
OS      Caspase.
GN      CASPA OR CASPY.
OC      Brachydanio rerio (Zebrafish) (Danio rerio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OX      Cyprinidae; Danio.
OX      NCBI_Taxid=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=20373792; PubMed=10917738;
RA      Inohara N., Nunez G.;
RT      "Genes with homology to mammalian apoptosis regulators identified in
RT      zebrafish.";
RL      Cell Death Differ. 7:509-510(2000).
DR      EMBL; AF233434; AAC66964.1; -.
DR      HSP; P29466; IICE.
DR      ZFIN; ZDB-GENE-000616-3; caspa.
DR      GO; GO:0030693; F:caspase activity; IEA.
DR      GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR      InterPro; IPR002138; ICE p10.
DR      InterPro; IPR001309; ICE p20.
DR      InterPro; IPR004020; PAAD DAPIIN dom.
DR      InterPro; IPR002398; Peptidase_C14.
DR      Pfam; PF02758; PAAD DAPIIN; 1.
DR      Pfam; PF00656; Peptidase_C14; 1.
DR      PRINTS; PR00376; IL1BCENZME.
DR      SMART; SM00115; CASc; 1.
DR      PROSITE; PS01122; CASPASE_CYS; 1.
DR      PROSITE; PS01121; CASPASE_HIS; 1.
DR      PROSITE; PS50207; CASPASE_P10; 1.
DR      PROSITE; PS50208; CASPASE_P20; 1.
DR      PROSITE; PS50824; DAPIIN; 1.
SQ      SEQUENCE 383 AA; 43966 MW; 21890871309774C3 CRC64;

```

Query Match 22.2%; Score 274.5; DB 13; Length 383;
Best Local Similarity 30.0%; Pred. No. 4, 7e-15;
Matches 69; Conservative 49; Mismatches 83; Indels 29; Gaps 6;

```

QY      29 RSGSEEDLALHMFQRLRFSTMKRDPYAEQOELEKFAQALDSREDPVSCAFVYMA 88
Db      162 RSGSEKDEENMKELKELDYQVVKRPLSAKENDAIKDPAQREHKKYS--DSAFVYMS 219
QY      89 HGESEGFLKGGDEGMVLENTLFEALNNKCOALRAKPKYVITIOACRGEGRDPG-ETVGGDE 137
Db      220 HGRKDAIKGVNHNRTNNPDSFVVDVNYRLNSKCPALDKRKVILIOACRGEGRGRVW 279
QY      138 ----DGEVVGDEIYVWIKDSQOTIPYTDALHVVSTYEGYIAYRHDKGSCFIOTLVDP 193
Db      280 ASDGEEDPELEIDDDDFVHKK-----DFISLMSCPDPTSKSYHVQNGTGYVQTLVD 331
QY      194 VFTRK--RKXHILELITEVTRMAEALVQEGKARKTNPEIQTSTARKRY 241
Db      332 VFTRKAEHDIHELFRKVLIRFEHFNMT--GNFKQACRDRATLPLFYIL 379

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RESULT 13

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ID      08CHV5      PRELIMINARY;      PRT;      313 AA.
AC      08CHV5;
DT      01-MAR-2003 (Tremblrel. 23, Created)
DT      01-MAR-2003 (Tremblrel. 23, Last sequence update)
DE      01-OCT-2003 (Tremblrel. 25, Last annotation update)
OS      Caspase 3, apoptosis related cysteine protease (Fragment).
GN      CASP3.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RA Strausberg R.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC038825; AAH38825.1; -.
DR MGI; MGI:107739; Casp3.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCNZYME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR Protease.
FT NON_TER.
SQ SEQUENCE 313 AA; 35174 MW; 96E98A1F04E769FC CRC64;

Query Match 22.1%; Score 273.5; DB 11; Length 313;
Best Local Similarity 34.8%; Pred. No. 4.4e-15;
Matches 77; Conservative 34; Mismatches 93; Indels 17; Gaps 7;

QY 28 ARGESEDDALHEMRQLRFESTMRDPTAEFOFELEKFOQALISREDPVCARVYM 87
DB 99 SRSGTVDANILKETTNGKLYQVRNKNDLTREDILBMDSVSKDSKSSFFVC---VII 155
QY 88 AHGREGLKEDGEMVYKLENTLFEALNNKNCALRAKPKVYIIQACRGEQDPG-ETVGGD 146
DB 156 SHGDSGVITVTNGP-VELKGLTFPRGDDYCRSLTKRKLFTIQAQCTEIDCGIETDSCGT 214
QY 147 EIVWVKDSPQITPTVTDALHVSIVTEGYIAYRHQDGKSCFIQTLVDVFTKRKHILE-- 204
DB 215 DEEMAC---QKIPVEADFLIYASTAGYSWRNKSGWFIQSLCSML-KLYAHKLEFM 269
QY 205 -LITEVTRMA---EAEIVQEGKAKRTNEIQTSLAKRLY 240
DB 270 HILTRVRKVAETEFEPSLDSFTFAKKQIPICIIVSMITKELY 310

RESULT 14
Q8MK15 PRELIMINARY; PRT; 277 AA.
AC Q8MK15;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Caspase-3.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Carnivora; Fissipedia; Canidae; Canis.
OX NCB1_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Sano J.;
RT "canine Caspase-3 gene."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB085580; BAB92962.1; -.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001309; ICE_p10.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCNZYME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.

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DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 277 AA; 31334 MW; 7094C76D868DBA9 CRC64;

Query Match 22.0%; Score 272.5; DB 6; Length 277;
Best Local Similarity 33.5%; Pred. No. 4.6e-15;
Matches 84; Conservative 32; Mismatches 108; Indels 27; Gaps 9;

QY 9 EEKYMSGAMALILCVTK-----AREGESEDDALHEMRQLRFESTMRDPTA 58
DB 34 DNSYKMDYEMELCIINNNKNNFKSTGMAPRSGTVDANILKETFTNLXYEVNKNNDLTC 93
QY 59 EFOFELEKFOQALISREDPVCARVYMAHREBEGLKEDGEMVYKLENTLFEALNNKNCQ 118
DB 94 EELILEMNSVSKDSKSSFFVC---VLLSHDEGIIFTNGP-VDLRKVTGPFRGDYCR 149
QY 119 ALRAKPKVYIIQACRGEQDPG-ETVGGDEIWMVKDSPQITPTVTDALHVSIVTEGYIA 177
DB 150 SLTGKPKLFTIQAQCTEIDCGIETDSCIEDMAC---QKIPVEADFLIYASTAGYYS 205
QY 178 YRHQDGKSCFIQTLVDVFTKRKHILE--LITEVTRMA-EAEIVQEGKA--KRTNP 230
DB 206 WNSKXGSMFIQSLC-AMKLYAHKLEFPHILTRVRKVAETEFEPSLDSAFHKKQIP 264
QY 231 IOSTLRKRLYL 241
DB 265 IVSMLYKEDLYL 275

RESULT 15
Q91B63 PRELIMINARY; PRT; 399 AA.
AC Q91B63;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Caspase-9.
GN XCASPASE-9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCB1_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20209426; Pubmed=10744739;
RA Nakajima K., Takahashi A., Yacita Y.;
RT "structure, expression and function of the Xenopus laevis caspase
family."
RL J. Biol. Chem. 275:10484-10491 (2000).
DR EMBL; AB038172; BAA94750.1; -.
DR HSSP; Q15806; IQDU.
DR MEROPS; C14.010; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR004488; Death.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCNZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.

```

DR PROSITE, PS50207; CASPAGE_P10; 1.
 DR PROSITE, PS50208; CASPAGE_P20; 1.
 DR PROSITE, PS50017; DEATH_DOMAIN; 1.
 SQ SEQUENCE 399 AA; 44772 MW; EE2A269719064F9F CRC64;

Query Match 22.0%; Score 272; DB 13; Length 399;
 Best Local Similarity 27.9%; Pred. No. 8e-15;

Matches 80; Conservative 40; Mismatches 107; Indels 60; Gaps 8;

QY 2 SNPRSLIEEK-YDMGALALILICVT-----KARSGSEEDLALHEMFQARFES 50
 Db 125 SRKGTLDKDXPKMSSDPDIFGCLINNNNFHECTGLSTRGSDIDRDLANKRMSFFHEV 184
 QY 51 TMKRDPTAEQFOEILEKFOQAIDSRNEDPVSCAFVVLMAHGRE-----GFLKGECDGEMV 103
 Db 185 TVKDNLTGQAMHDHLOALADQDHSIQD---CCLVVIISHGCETRHIGFPGGVYGTGIRI 241
 QY 104 KLENLFEALNNKNGQALRAKPKVYTIQACRGEQDPEGTVG----- 145
 Db 242 PVERIVSYFNGSKCPSLKGPKEKIFLIQACGSDQDKGCEVTSETPPLSPSTSLQSDATP 301
 QY 146 -----DEIVWYIKDSPQTIPTYPDALHYSTVEGYIAYRHDOKSGCFIQTLVDVFTK 197
 Db 302 VFSGEGRDEV-----DAVSNIPTPSDILVYSTFPQVSWRDKHGTGSMWYEVLDVLAE 356
 QY 198 RKG--HILELITEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYLQ 242
 Db 357 HAAADDLQSLVWV-----ADGVSSKGTYKQIPGYFNFLEKRFYFK 397

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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:39:36 ; Search time 43.438 Seconds
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Title: US-10-068-564-5_COPY_1_146
Perfect score: 752
Sequence: 1 MSNPRSLREKXDMGAAIA.....YTIQACRGQRDPGETVGD 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2002s:*
6: geneseq2003as:*
7: geneseq2003bs:*
8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match Length	ID	Description
1	747	99.3	230 3 AAY93215	AAY93215 Amino aci
2	747	99.3	242 3 AAY93214	AAY93214 Amino aci
3	747	99.3	242 5 AAG77980	AAG77980 Full-len
4	702	93.4	242 5 AAG77984	AAG77984 Full-len
5	679	90.3	229 3 AAY68865	AAY68865 Amino aci
6	586	77.9	257 3 AAY68864	AAY68864 Amino aci
7	586	77.9	281 3 AAY93592	AAY93592 Mouse cas
8	586	77.9	281 3 AAY93216	AAY93216 Amino aci
9	578	76.9	214 3 AAY93213	AAY93213 Amino aci
10	300.5	40.0	234 5 AAU72882	AAU72882 Human asp
11	300.5	40.0	398 5 ABG76499	ABG76499 DNA encod
12	210	27.9	435 2 AAR66771	AAR66771 Human int
13	210	27.9	435 2 AAR98462	AAR98462 Human ice
14	210	27.9	435 2 AAR90703	AAR90703 Interleuk
15	210	27.9	435 2 AAM26274	AAM26274 Cell deat
16	210	27.9	435 2 AAY21716	AAY21716 Amino aci
17	210	27.9	435 2 AAB14257	AAB14257 Human ich
18	210	27.9	435 4 AAE00599	AAE00599 Human cas
19	210	27.9	435 5 ABB78321	ABB78321 Amino aci
20	210	27.9	435 5 ABB01217	ABB01217 Human cas
21	210	27.9	435 7 ADE63002	ADE63002 Human pro
22	210	27.9	441 2 AAR66768	AAR66768 Human int
23	210	27.9	441 3 AAB14253	AAB14253 Human ich
24	207	27.5	452 5 ABB10110	ABB10110 Mouse cas
25	205	27.3	452 7 ADB79812	ADB79812 Rat caspa

26	205	27.3	452 7 ADE63000	ADE63000 Rat Prote
27	197	26.2	312 2 AAR66772	AAR66772 Human int
28	197	26.2	312 2 AAR98463	AAR98463 Human ice
29	197	26.2	312 3 AAB14258	AAB14258 Human ich
30	197	26.2	312 4 AAE00616	AAE00616 Human cas
31	197	26.2	312 5 AAU96868	AAU96868 Human cas
32	197	26.2	457 4 AAM25766	AAM25766 Human pro
33	196	26.1	435 3 AAB14262	AAB14262 Mutant hu
34	190.5	25.3	250 4 AAB98653	CAspase-1
35	189	25.1	404 2 AAU01315	AAU01315 Canine in
36	189	25.1	404 3 AAY82559	AAU82559 Canine in
37	189	25.1	404 3 AAY82561	AAU82561 Canine in
38	187.5	24.9	256 4 AAB59580	AAU59580 Human cas
39	187.5	24.9	311 2 AAM00994	AAU00994 Interleuk
40	187.5	24.9	323 2 AAM00988	AAU00988 Human int
41	187.5	24.9	339 2 AAM00989	AAU00989 Human int
42	187.5	24.9	383 2 AAM00993	AAU00993 Interleuk
43	187.5	24.9	383 4 AAE00615	AAE00615 Human cas
44	187.5	24.9	394 2 AAR33779	AAU33779 ICE. 3/20
45	187.5	24.9	404 2 AAR15745	AAR15745 Interleuk

ALIGNMENTS

RESULT 1	AAU93215	standard; protein; 230 AA.
ID	AAU93215	
XX	AAU93215;	
AC		
XX		
DT	04-SRP-2000 (first entry)	
XX		
DE	Amino acid sequence of a human caspase-14 splice variant.	
XX		
KM	Caspase-14; cell death specific protease; apoptosis stimulator;	
KW	apoptosis; AIDS; neurodegenerative disease; ischemic injury.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Active-site	130..134
XX		
PN	WO200028047-A1.	
XX		
PD	18-MAY-2000.	
XX		
PF	29-OCT-1999; 99WO-US025523.	
XX		
PR	06-NOV-1998; 98US-00187789.	
XX	(UYJE-) UNIV JEFFERSON THOMAS.	
PA		
XX		
XX	Alnemri ES, Fernandez-Alnemri T;	
PI		
XX	WPI; 2000-376558/32.	
DR	N-PSDB; AAA15165.	
XX		
PT	Novel nucleic acids encoding cell death specific protease termed caspase-14 useful for treating cancers by stimulating apoptosis.	
XX		
PS	Claim 41; Fig 8; 78pp; English.	
XX		
CC	The present sequence represents a human caspase-14 splice variant. The polypeptide is a cell death specific protease, and is an apoptosis stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase-14 antibodies are useful for treating or reducing the severity of pathological conditions associated with increased or decreased levels of apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative diseases and ischemic injury are treated by administering anti-caspase-14 antibodies. The antibody is useful for determining the presence of the level of caspase-14 in tissue sample and also for the isolation of caspase-14 with apoptotic activity or in screening assay to identify an	

CC agent that inhibits heterodimer or heterotetramer formation and
CC therefore, apoptosis
XX
SQ Sequence 230 AA;

Query Match 99.3%; Score 747; DB 3; Length 230;
Best Local Similarity 99.3%; Pred. No. 7.4e-76;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPSLEEEKYDMSGALALILCTKARSGSEEDLDLEHMFRLRRESTMKRPTAEQ 60
Db 1 MSNPSLEEEKYDMSGALALILCTKARSGSEEDLDLEHMFRLRRESTMKRPTAEQ 60
QY 61 FOEIEKFOQAIDSRDPVSCAFVYLMHAGREGFLKSGDGMVKLENFEALNNKCOAL 120
Db 61 FOEIEKFOQAIDSRDPVSCAFVYLMHAGREGFLKSGDGMVKLENFEALNNKCOAL 120
QY 121 RAKPKVYIIQACRGEQRDPGETVGSD 146
Db 121 RAKPKVYIIQACRGEQRDPGETVGSD 146

RESULT 2

AAV93214 standard; protein; 242 AA.

04-SEP-2000 (first entry)

Amino acid sequence of a human caspase-14.

Caspase-14; cell death specific protease; apoptosis stimulator;
apoptosis; AIDS; neurodegenerative disease; ischemic injury.

Homo sapiens.

Key Location/Qualifiers
Region 1..146
Active-site 130..134
Cleavage-site 146..147
Region 147..242
/note= "small subunit"

MO200028047-A1.

18-MAY-2000.

29-OCT-1999; 99WO-US025523.

06-NOV-1998; 98US-00187789.

(UYJE-) UNIV JEFFERSON THOMAS.

Alnemri ES, Fernandez-Alnemri T;

WPI; 2000-376558/32.

N-PSDB; AAA15164.

Novel nucleic acids encoding cell death specific protease termed caspase-14 useful for treating cancers by stimulating apoptosis.

Claim 13; Fig 7; 78pp; English.

The present sequence represents a human caspase-14 polypeptide. The polypeptide is a cell death specific protease, and is an apoptosis stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase-14 antibodies are useful for treating or reducing the severity of pathological conditions associated with increased or decreased levels of apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative diseases and ischemic injury are treated by administering anti-caspase-14 antibodies. The antibody is useful for determining the presence or the

CC level of caspase-14 in tissue sample and also for the isolation of
CC caspase-14 with apoptotic activity or in screening assay to identify an
CC agent that inhibits heterodimer or heterotetramer formation and
CC therefore, apoptosis
XX
SQ Sequence 242 AA;

Query Match 99.3%; Score 747; DB 3; Length 242;
Best Local Similarity 99.3%; Pred. No. 7.9e-76;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPSLEEEKYDMSGALALILCTKARSGSEEDLDLEHMFRLRRESTMKRPTAEQ 60
Db 1 MSNPSLEEEKYDMSGALALILCTKARSGSEEDLDLEHMFRLRRESTMKRPTAEQ 60
QY 61 FOEIEKFOQAIDSRDPVSCAFVYLMHAGREGFLKSGDGMVKLENFEALNNKCOAL 120
Db 61 FOEIEKFOQAIDSRDPVSCAFVYLMHAGREGFLKSGDGMVKLENFEALNNKCOAL 120
QY 121 RAKPKVYIIQACRGEQRDPGETVGSD 146
Db 121 RAKPKVYIIQACRGEQRDPGETVGSD 146

RESULT 3

AAG77980 standard; protein; 242 AA.

AAG77980;

05-APR-2002 (first entry)

Full-length human caspase-14.

Human; caspase-14; anti-apoptotic; apoptosis.

Homo sapiens.

WO200181595-A2.

01-NOV-2001.

27-APR-2001; 2001WO-US013831.

27-APR-2000; 2000US-019962P.

(KNOL) KNOLL GMBH.

Mankovich JA;

WPI; 2002-041410/05.

N-PSDB; AAK98248.

Novel isolated human caspase-14 proteins and nucleic acid sequences, useful for identifying modulators of caspase-14 protein that are useful for modulating apoptosis.

Claim 20; Fig 1; 58pp; English.

The sequence represents the novel full-length human caspase-14 protein, referred to as "Caspase-14 NEW" in the specification. The invention relates to a novel isolated human caspase-14 protein comprising an amino acid sequence with MSNPSLE, at its amino terminus. The caspase-14 of the invention has anti-apoptotic activity. Caspase-14 acts as a modulator of caspase-14 activity. The polypeptide is useful for identifying a compound which is a modulator of human caspase-14 activity, and is also useful for identifying a compound which modulates the interaction of caspase-14 with a target molecule. An antibody to caspase-14 is useful for isolating the protein by standard techniques, and for detecting caspase-14 to evaluate the abundance and expression pattern. The antibody is also useful for diagnostically monitoring protein levels in a tissue as a part of a clinical testing procedure. The polypeptide is useful as a protease to cleave substrates and for inducing apoptosis in cells, in

CC screening assays, and as a bait protein in a two-hybrid or three-hybrid
CC assay to identify other proteins that interact with human caspase-14
CC protein
XX
SQ Sequence 242 AA;

Query Match 99.3%; Score 747; DB 5; Length 242;
Best Local Similarity 99.3%; Pred. No. 7.9e-76;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPSRLSEEEKYDMSGALALILCYTKAREGSEDDDLAEMHPRQLRFESTMKRDPDTAQ 60
DB 1 MSNPSRLSEEEKYDMSGARALILCYTKAREGSEDDDLAEMHPRQLRFESTMKRDPDTAQ 60
QY 61 FQBELLEKFOAIDSRDPVSCAFVVLMAHGREGFLKGEDEGVKLENLFEALNNKCOAL 120
DB 61 FQBELLEKFOAIDSRDPVSCAFVVLMAHGREGFLKGEDEGVKLENLFEALNNKCOAL 120
QY 121 RAKPKYIIIOACRGEQRPGETVGGD 146
DB 121 RAKPKYIIIOACRGEQRPGETVGGD 146

RESULT 4
AAG7984
ID AAG7984 standard; protein; 242 AA.
XX
AC AAG7984;
XX
DT 05-APR-2002 (first entry)
XX
DE Full-length human caspase-14 old.
XX
KM Human; caspase-14; anti-apoptotic; apoptosis.
XX
OS Homo sapiens.
XX
PN WO200181595-A2.
XX
PD 01-NOV-2001.
XX
PF 27-APR-2001; 2001WO-US013831.
XX
PR 27-APR-2000; 2000US-0199962P.
XX
PA (KNOL) KNOLL GMBH.
XX
PI Mankovich JA;
XX
DR WPI; 2002-041410/05.
XX
PT Novel isolated human caspase-14 proteins and nucleic acid sequences,
PT useful for identifying modulators of caspase-14 protein that are useful
PT for modulating apoptosis.
XX
PS Example; Fig 1; 58pp; English.
XX

CC The sequence represents the full-length human caspase-14 protein,
CC referred to as "Caspase-14 OLD" in the specification. The invention
CC relates to a novel isolated human caspase-14 protein comprising an amino
CC acid sequence with MSNPSRLSE, at its amino terminus. The caspase-14 of
CC the invention has anti-apoptotic activity. Caspase-14 acts as a modulator
CC of caspase-14 activity. The polypeptide is useful for identifying a
CC compound which is a modulator of human caspase-14 activity, and is also
CC useful for identifying a compound which modulates the interaction of
CC caspase-14 with a target molecule. An antibody to caspase-14 is useful
CC for isolating the protein by standard techniques, and for detecting
CC caspase-14 to evaluate the abundance and expression pattern. The antibody
CC is also useful for diagnostically monitoring protein levels in a tissue
CC as a part of a clinical testing procedure. The polypeptide is useful as a
CC protease to cleave substrates and for inducing apoptosis in cells, in
CC screening assays, and as a bait protein in a two-hybrid or three-hybrid
CC assay to identify other proteins that interact with human caspase-14

CC protein
XX
SQ Sequence 242 AA;

Query Match 93.4%; Score 702; DB 5; Length 242;
Best Local Similarity 99.3%; Pred. No. 9.6e-71;
Matches 136; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 EKYDMSGALALILCYTKAREGSEDDDLAEMHPRQLRFESTMKRDPDTAQEQBELLEKQ 69
DB 10 EKYDMSGARALILCYTKAREGSEDDDLAEMHPRQLRFESTMKRDPDTAQEQBELLEKQ 69
QY 70 QALDSREDPVSCAFVVLMAHGREGFLKGEDEGVKLENLFEALNNKCOALRAKPKYII 129
DB 70 QALDSREDPVSCAFVVLMAHGREGFLKGEDEGVKLENLFEALNNKCOALRAKPKYII 129
QY 130 QACRGEQRPGETVGGD 146
DB 130 QACRGEQRPGETVGGD 146

RESULT 5
AAY68865
ID AAY68865 standard; protein; 229 AA.
XX
AC AAY68865;
XX
DT 16-MAY-2000 (first entry)
XX
DE Amino acid sequence of a human caspase-like polypeptide.
XX
KM Mouse; caspase-like polypeptide; human; caspase; apoptosis; skin disease;
KM keratinisation; wound healing.
XX
OS Homo sapiens.
XX
PN WO200004169-A1.
XX
PD 27-JAN-2000.
XX
PF 12-JUL-1999; 99WO-EP004939.
XX
PR 17-JUL-1998; 98EP-00202422.
XX
PA (VLAAS-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI Van De Craen M, Declercq W, Vandenaabeele P, Fliers W;
XX
DR WPI; 2000-182433/16.
XX
DR N-PSDB; AAZ60684.
XX
PT New murine and human caspase homologues useful for treating skin related
PT disorders.
XX
PS Claim 2; Page 53-54; 68pp; English.
XX

CC The present sequence represents a human caspase-like polypeptide. The
CC specification also describes a murine caspase-like polypeptide. Caspases
CC are cysteine/aspartate-specific proteinases which play a central role in
CC apoptosis. The polypeptides of the invention are related to human and
CC murine caspase-2 and human caspase-9, and possess all of the typical
CC amino acids involved in catalysis, including the QACRG box, and contain
CC no or only a very short prodomain. mRNA expression of the homologues of
CC the invention is predominant in the skin. The caspase-like polypeptides
CC are useful for treating human or animal diseases, such as skin diseases.
CC They are also useful for screening for compounds that modulate its
CC activity, i.e. agonists, antagonists, and inhibitors. The caspase-like
CC polypeptides and polynucleotides are useful for modulating
CC keratinisation, for diagnosing and treating inappropriate wound healing
CC
SQ Sequence 229 AA;

Query Match 90.3%; Score 679; DB 3; Length 229;

Best Local Similarity 99.2%; Pred. No. 3,6e-68;
Matches 132; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Dy 14 MSGALALLICVTKAREGSEEDDLAIEHMFQRLRFESTMKDPTAEQFOEELFKFOCALD 73
|||
Db 1 MSGARLALLICVTKAREGSEEDDLAIEHMFQRLRFESTMKDPTAEQFOEELFKFOCALD 60

Db 61 SRELPVSCAFVLMAHGREGLKGEDEGMVLTLENLEFALNNNCQALRAKPKYIIQACR 120

OY	134 GEORDPGETVGGD	146
Dd	121 GEORDPGETVGGD	133

RESULT 6
AAy68864
ID AAy68864 standard; protein; 257 AA.
yy

AC	AAV68864;
XX	
DT	16-MAY-2000 (first entry)

XX
DE Amino acid sequence of a murine caspase-like polypeptide.
XX
XXXXXX

OS Mus musculus.

XX	.
PN	WO200004169-A1.
XX	
27	JAN 2000

XX 12-JUL-1999; 99WO-EP004939.
PF
XX

PR 17-JUL-1998; 98EP-00202422.
XX
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX

PI Van De Craen M, Declercq W, Vandenabele P, Fiers W;
XX
DR WPI: 2000-182433/16.

DR N-PSDB; AAZ60683.
XX
PT New murine and human caspase homologues useful for treating skin related
disorders

XX
PS
XX
Claim 1; Page 51-52; 68pp; English.

The present sequence represents a murine caspase-like polypeptide. The specification also describes a human caspase-like polypeptide. Caspases are cysteine1 aspartate-specific proteinases which play a central role in apoptosis. The

murine caspase-2 and human caspase-9, and possess all of the typical amino acids involved in catalysis, including the QACGG box, and contain no or only a very short prodomain. mRNA expression of the homologue of

the invention is predominant in the skin. The caspase-like polypeptides are useful for treating human or animal diseases, such as skin diseases. They are also useful for screening for compounds that modulate its

keratinisation, for diagnosing and treating inappropriate wound healing

Query Match	77.9%	Score 586;	DB 3;	Length 257;
Post Local	75.0%			
Sequence 257 AA;				

MSNPRLSEEEKYDMSGAAATATTCCTKARQSGFEDTALFHMEROI DEESTWVRDNNATNO 60
Matches 111; Conservative 18; Mismatches 17; Indels 0; Gaps 0;

[illegible]

D_b 5 MSDFQPLQEBRYDMGALIALTLCTKAREGEVDMEALERMFRYLKFESTMKRDPTAQQ 64

61 FQEELEKFOALIDREDPVSCAFVILMAHGEBGLNGEDGEVKKENTLFEALNNKKCAL 120
| | | : | | | : : | | | | | | | | | | : | | | : |
Db 65 FLBELDEFQOTIDNWEPEVSCAFVILMAHGEGGLNGEDEKVRLEDLFVLNNKKCAL 124

D_b 125 R G K P K V Y I I Q A C R G E H R D P G E E L R G N 150

RESULT 7
AAW93592
ID AAW02503

XX 21-JUN-1999 (first entry)

DE Mouse caspase-14 protein.
XX
KW Caspase-14; murine; protease; treatment; apoptotic-related disease;

KM acquired immunodeficiency syndrome; AIDS;
 KM autoimmune disease; cancer;
 KM neurodegenerative disease; ischemic injury; anti-idiotypic antibody;
 KM caspase-14 processing activity; epitope; competitor; modulator.

OS	Mus sp.
XX	
PN	W0910504-A2.
...	

04-MAR-1999.
XX
26-AUG-1998 : 98WO-11S017715
PF

XX
PR 26-AUG-1997; 97US-0056986P.
XX

XX
PI Alnemri ES, Fernandes-Alnemri T;
XX

DR WPI; 1999-204670/17.
DR N-PsDB; AAX23515.
XX

newly isolated polynucleotide encoding a caspase-14 polypeptide - useful for identifying (ant)agonists that are useful in the diagnosis and treatment of apoptosis-related diseases.

PS Claim 4; Fig 1, 59pp, English.
XX
CC This invention describes a novel murine caspase-14 which has protease
XX activity.

CC (ant) agonists of the polypeptide, where enzyme activity is measured with
CC a fluorescent substrate (especially DEVD-AMC or YVAD-AMC. Activated
CC caspase-14 is useful for identifying inhibitors or enhancers of caspase

14 actively. The compounds identified by both methods form pharmaceutical compositions for treating apoptotic-related diseases, including autoimmune disease, cancer, acquired immunodeficiency syndrome (AIDS),

antibody is useful for measuring the level of caspase-14 in a tissue sample. An antibody that binds to a caspase-14 polypeptide is useful for isolating the polypeptide, and an antibody that binds to the larva or

small subunit the polypeptide is useful for identifying samples with caspase-14 processing activity. An antibody that binds to caspase-14 heterodimer or heterotetramer is useful for isolating caspase-14 with

antibodies form kits for such purposes. The anti-caspase-14 antibody is also useful for preparing anti-idiotypic antibodies, which mimic a caspase-14 epitope recombinized by the anti-caspase-14 antibody, therefore

the antibody is useful as a competitor of caspase-14 in reducing the level of caspase-14 activity, which reduces the level of apoptotic activity. Oligonucleotides made from the polynucleotides are useful as

cDNA libraries for similar caspase-14 encoding polynucleotides, or for polymerase chain reaction (PCR) primers or probes to screen genomic or cDNA libraries for similar caspase-14 encoding polynucleotides, or for

CC diagnosis of diseases associated with enhanced or inhibited apoptosis.
CC The isolated caspase-14 gene permits methods of modulating apoptosis for
CC the treatment of human diseases
XX
SQ Sequence 281 AA;

Query Match 77.9%; Score 586; DB 2; Length 281;
Best Local Similarity 76.0%; Pred. No. 1.5e-57;
Matches 111; Conservative 18; Mismatches 17; Indels 0; Gaps 0;

QY 1 MSNPRLSEEEKYMGSAIALILICVTKARGSEEDIDALEHMRQLRPFSTMKRDPDTAQ 60
DB 24 MSDPQLQEBRYMGSARIALTLICVTKARGSEVDMEALERMRYLKFSSTMKRDPDTAQ 83
QY 61 FOEELKFOADISREDPVSCAFVVMARGREGFLKGEDEGVKLENTLEFALNNKXCOAL 120
DB 84 FLEELDEFQOTIDNMEEPVSCAFVVMARGREGFLKGEDEGVKLENTLEFALNNKXCKL 143
QY 121 RAKPKYIIIOACRGEGQDPGETVGS 146
DB 144 RGRPKYIIIOACRGHRDPGEELRGN 169

RESULT 8

AA93213
ID AAY93213 standard; protein; 281 AA.

AC AAY93213;

XX 04-SEP-2000 (first entry)

XX Amino acid sequence of a murine caspase-14.

XX Caspase-14; cell death specific protease; apoptosis stimulator;

KW apoptosis; AIDS; neurodegenerative disease; ischemic injury.

OS Mus sp.

XX Key Location/Qualifiers

FT Region

FT Active-site

FT Cleavage-site

FT Cleavage-site

FT Region

FT /note= "small subunit"

XX WO200028047-A1.

XX 18-MAY-2000.

XX 29-OCT-1999; 99WO-US025523.

XX 06-NOV-1998; 98US-00187789.

XX (UYJB-) UNIV JEFFERSON THOMAS.

XX Alnemri ES, Fernandez-Alnemri T;

XX WPI; 2000-376558/32.

XX N-PSDB; AAA15163.

XX Novel nucleic acids encoding cell death specific protease termed caspase-14 useful for treating cancers by stimulating apoptosis.

XX Claim 52; Fig 1; 78pp; English.

XX The present sequence represents a murine caspase-14 polypeptide. The polypeptide is a cell death specific protease, and is an apoptosis stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase-14 antibodies are useful for treating or reducing the severity of pathological conditions associated with increased or decreased levels of apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative

CC diseases and ischemic injury are treated by administering anti-caspase-14
CC antibodies. The antibody is useful for determining the presence of the
CC level of caspase-14 in tissue sample and also for the isolation of
CC caspase-14 with apoptotic activity or in screening assay to identify an
CC agent that inhibits heterodimer or heterotetramer formation and
CC therefore, apoptosis

XX Sequence 281 AA;

Query Match 77.9%; Score 586; DB 3; Length 281;
Best Local Similarity 76.0%; Pred. No. 1.5e-57;
Matches 111; Conservative 18; Mismatches 17; Indels 0; Gaps 0;

QY 1 MSNPRLSEEEKYMGSAIALILICVTKARGSEEDIDALEHMRQLRPFSTMKRDPDTAQ 60
DB 24 MSDPQLQEBRYMGSARIALTLICVTKARGSEVDMEALERMRYLKFSSTMKRDPDTAQ 83
QY 61 FOEELKFOADISREDPVSCAFVVMARGREGFLKGEDEGVKLENTLEFALNNKXCOAL 120
DB 84 FLEELDEFQOTIDNMEEPVSCAFVVMARGREGFLKGEDEGVKLENTLEFALNNKXCKL 143
QY 121 RAKPKYIIIOACRGEGQDPGETVGS 146
DB 144 RGRPKYIIIOACRGHRDPGEELRGN 169

RESULT 9

AA93216
ID AAY93216 standard; protein; 214 AA.

AC AAY93216;

XX 04-SEP-2000 (first entry)

XX Amino acid sequence of a human caspase-14 splice variant.

XX Caspase-14; cell death specific protease; apoptosis stimulator;

KW apoptosis; AIDS; neurodegenerative disease; ischemic injury.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Active-site

FT Active-site

XX WO200028047-A1.

XX 18-MAY-2000.

XX 29-OCT-1999; 99WO-US025523.

XX 06-NOV-1998; 98US-00187789.

XX (UYJB-) UNIV JEFFERSON THOMAS.

XX Alnemri ES, Fernandez-Alnemri T;

XX WPI; 2000-376558/32.

XX N-PSDB; AAA15166.

XX Novel nucleic acids encoding cell death specific protease termed caspase-14 useful for treating cancers by stimulating apoptosis.

XX Claim 42; Fig 9; 78pp; English.

XX The present sequence represents a human caspase-14 splice variant. The polypeptide is a cell death specific protease, and is an apoptosis stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase-14 antibodies are useful for treating or reducing the severity of pathological conditions associated with increased or decreased levels of apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative diseases and ischemic injury are treated by administering anti-caspase-14 antibodies. The antibody is useful for determining the presence or the level of caspase-14 in tissue sample and also for the isolation of

CC caspase-14 with apoptotic activity or in screening assay to identify an
CC agent that inhibits heterodimer or heterotrimer formation and
CC therefore, apoptosis

XX Sequence 214 AA;

Query Match 76.9%; Score 578; DB 3; Length 214;
Best Local Similarity 80.1%; Pred. No. 8.5e-57;
Matches 117; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MSNRSLSLEEKYKMSGALALILCYTKARSGSEEDLDALHEMFRLQRPSTMKEDPTAAEQ 60
DB 1 MSNRSLSLEEKYKMSGALALILCYTKARSGSE----- 34

QY 61 FOEELERFOQALIDREDPVSCAFVYLMAHGREGFLKGEDGEMVLENTLEALNNKCOAL 120
DB 35 --EELERFOQALIDREDPVSCAFVYLMAHGREGFLKGEDGEMVLENTLEALNNKCOAL 92

QY 121 RAKPKVYIIQACRGEGQDPGRTVGAD 146
DB 93 RAKPKVYIIQACRGEGQDPGRTVGAD 118

RESULT 10

ID AAU72882 standard; protein; 234 AA.

XX AAU72882;

DT 26-FEB-2002 (first entry)

DE Human aspartyl protease partial protein sequence #7.

XX Human; protease; PCR primer; cytosolic; immunomodulator; cardiac;
KM vasotrophic; antidiarrheal; analgesic; endocrine; nootropic; tranquiliser;
KM hypertensive; hypotensive; neuroleptic; neuroprotective; anabolic;
KM antiretic; antiinflammatory; aspartyl protease; cysteine protease;
KM metalloprotease; serine protease; cancer; haematopoietic; breast; colon;
KM lung; prostate; cervical; brain; ovarian; bladder; kidney; pain;
KM immune-related disease; cardiovascular disease; neuronal disease;
KM migraine; sexual dysfunction; mood disorder; attention disorder;
KM cognition disorder; hypotension; hypertension; psychotic disorder;
KM dyskinnesia; metabolic disorder; inflammatory disorder.

XX Homo sapiens.

XX MO200183782-A2.

XX 08-NOV-2001.

XX 04-MAY-2001; 2001MO-US014431.

XX 04-MAY-2000; 2000US-0201879P.

XX (SUGEN-) SUGEN INC.

XX Plozman GD, Whyte D, Sudarsanam S, Manning G, Caenepeel S;
PI Payne V;

XX MPI: 2002-041502/05.

XX N-FSDB; AAS97165.

XX Novel protease polypeptide useful for screening for substances that may
PT be used to treat, e.g., cancers, immune-related diseases, cardiovascular
PT disease, migraine, pain, psychotic and inflammatory disorders.

XX Claim 28; Fig 2A; 232DP; English.

XX The invention relates to an isolated, enriched, or purified protease
CC polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to
CC screen for substances (S) that may modulate its activity. Administering S
CC (which modulates protease activity in vitro) may be used to treat a
CC disease or disorder selected from cancers (e.g., of tissues, of blood or

CC haematopoietic origin, of the breast, colon, lung, prostate, cervical,
CC brain, ovarian, bladder or kidney), immune-related diseases and
CC disorders, cardiovascular disease, brain or neuronal-associated diseases
CC (e.g., central or peripheral nervous system diseases, migraine, pain,
CC sexual dysfunction, mood disorders, attention disorders, cognition
CC disorders, hypotension, hypertension, psychotic disorders, neurological
CC disorders and dyskinnesia), metabolic disorders and inflammatory
CC disorders. (I) may also be useful as a diagnostic tool for a disease or
CC disorder such as those above. AAU72882-AU72910 represent human protease
CC amino acid sequences of the invention

XX Sequence 234 AA;

Query Match 40.0%; Score 300.5; DB 5; Length 234;
Best Local Similarity 46.6%; Pred. No. 2.2e-25;
Matches 61; Conservative 28; Mismatches 39; Indels 3; Gaps 2;

QY 11 KYDMSGALALILCYTKARSGSEEDLDALHEMFRLQRPSTMKEDPTAOROELEKREQ 70
DB 1 QYDLSKARALLILAVIGRGEGACHDVVALGGLCALGFEITVRIDPTAOROELEKPRE 60

QY 71 AIDSREDPVSCAFVYLMAH-GREGFLKGEDGEMVLENTLEALNNKCOALRAKPKYII 129
DB 61 QLDTCRGVPVSCAFVYLMAHGGRGQLIGADQGVQVPEALNQELS--RCQVIGRPKIFL 118

QY 130 QACRGEGQDPG 140
DB 119 QACRGEGQDPG 129

RESULT 11

ID ABG76499 standard; protein; 398 AA.

XX ABG76499;

DT 05-NOV-2002 (first entry)

DE DNA encoding protein modification and maintenance molecule #3.

XX Protein modification and maintenance molecule; gastrointestinal disorder;
KM dysphagia; esophageal spasm; gastritis; anorexia; nausea; hypertension;
KM cardiovascular disorder; atherosclerosis; vasculitis; aneurysm; allergy;
KM ischemic heart disease; autoimmune disorder; inflammatory disorder;
KM acquired immunodeficiency syndrome; AIDS; ankylosing spondylitis; cancer;
KM anaemia; amyloidosis; cell proliferative; arteriosclerotic bursts;
KM cirrhosis; developmental disorder; renal tubular acidosis; anaemia;
KM bone resorption; epilepsy; epithelial disorder; keratosis pilaris;
KM allergic contact dermatitis; insect bite; keloid; dermatofibroma; eczema;
KM Huntington's disease; stroke; cerebral neoplasm; Alzheimer's disease;
KM endometriosis; gynecomastia; ectopic pregnancy; gene therapy.

XX Homo sapiens.

XX MO200260942-A2.

XX 08-AUG-2002.

XX 30-JAN-2002; 2002MO-US002813.

XX 31-JAN-2001; 2001US-0265705P.

XX 05-FEB-2001; 2001US-0266762P.

XX 16-FEB-2001; 2001US-0269581P.

XX 23-FEB-2001; 2001US-0271198P.

XX 01-MAR-2001; 2001US-0272813P.

XX 13-MAR-2001; 2001US-0275586P.

XX 23-MAR-2001; 2001US-0278505P.

XX 30-MAR-2001; 2001US-0280539P.

XX (INCY-) INCYTE GENOMICS INC.

XX Warren BA, Honchell CD, Lu Y, Walia NK, Burford N, Delegeane AM;

XX (GEHO) GEN HOSPITAL CORP.
 PA Yuan J, Mura M;
 XX WPI; 1996-333763/33.
 DR N-PSDB; AAT31552.
 XX
 PT Preventing or promoting programmed cell death in vertebrate cells -
 PT computers inhibiting or increasing the activity of interleukin-1-beta
 PT converting enzyme, or altering expression of other related genes.
 PS Claim 19; Fig 10A; 127pp; English.
 XX
 CC A novel human cell death gene, designated Ich-1 (ICE-ced-3 homologue-1),
 CC was identified as a new member of the ced-3/ICE family. Ich-1 is
 CC alternatively spliced into 2 different forms. Ich-1L cDNA (AAT31552)
 CC encodes a 435-amino acid protein (AAR98462) that is homologous to the P20
 CC and P10 subunits of human interleukin-1 beta converting enzyme (ICE). Ich
 CC -1S cDNA (AAT31553) encodes a 312-amino acid protein (AAR98463) that is a
 CC truncated version of Ich-1L that terminates 21 residues after the QACRG
 CC fibroblast cells to die in culture, but overexpression of Ich-1L induces Rat-1
 CC suppresses Rat-1 cell death. Ich-1L and Ich-1S are useful in methods of
 CC controlling programmed cell death of vertebrate cells
 CC
 XX Sequence 435 AA;
 SQ
 Query Match 27.9%; Score 210; DB 2; Length 435;
 Best Local Similarity 37.5%; Pred. No. 8.6e-15;
 Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;
 QY 29 REGSEEDLALIEHMFQRLFEESTMKRDPETAEOFOEIEKFOQADISREDPVSCAFVYMA 88
 DB 202 RSGGDVHSTLVTLFKILGYDVHVLCDQTAGEMQEKIQNFAQ LPAHRVTDSC IVALIS 259
 QY 89 HGRBGFLEKGDENVKLENTPEALNNKQCALRAKPKVYIIOACRGQRDPG 140
 DB 260 HGVEGALYGVGKLLQLQEVFOLFNDNANCPSTLQNKPKMFFIOACRGDETDRG 311
 RESULT 14
 AAR90703
 ID AAR90703 standard; protein; 435 AA.
 AC AAR90703;
 XX
 DT 10-APR-1996 (first entry)
 XX
 DE Interleukin-1-beta converting enzyme like apoptosis protease-2.
 XX
 KW Interleukin-1-beta converting enzyme like apoptosis protease-2;
 KW ICE-LAP-2; cell death; immunosuppression; AIDS; Alzheimer disease;
 KW Parkinson disease; septic shock; rheumatoid arthritis; head injury;
 KW antitumor; antiviral.
 XX
 OS Homo sapiens.
 XX
 PN WO9600297-A1.
 XX
 PD 04-JAN-1996.
 XX
 PF 23-JUN-1994; 94WO-US007127.
 XX
 PR 23-JUN-1994; 94WO-US007127.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Wei WH, Craig AR, Hastings GA, Hudson PL, Kirkness EF;
 XX WPI; 1996-068881/07.
 DR N-PSDB; AAT15579.
 XX

PT Interleukin-1 beta converting enzyme like apoptosis protease-1 and -2 -
 PT controls programmed cell death, used in treatment of immunosuppression
 PT related disorders, e.g. AIDS and Alzheimer's disease.
 XX
 PS Claim 1; Fig 2A-C; 58pp; English.
 XX
 CC Human interleukin-1-beta converting enzyme like apoptosis protease-2 (ICE
 CC -LAP-2) (AAR90703) is structurally related interleukin-1-beta converting
 CC enzyme, which is responsible for apoptosis. Recombinant ICE-LAP-2 is
 CC obd. by expression of encoding cDNA (AAT15579) in prokaryotic or
 CC eucaryotic host cells. It is used to treat diseases related to abnormally
 CC controlled programmed cell death, to control vertebrate development and
 CC tissue homeostasis, to overcome viral infections and to treat
 CC immunosuppression-related disorders
 CC
 XX Sequence 435 AA;
 SQ
 Query Match 27.9%; Score 210; DB 2; Length 435;
 Best Local Similarity 37.5%; Pred. No. 8.6e-15;
 Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;
 QY 29 REGSEEDLALIEHMFQRLFEESTMKRDPETAEOFOEIEKFOQADISREDPVSCAFVYMA 88
 DB 202 RSGGDVHSTLVTLFKILGYDVHVLCDQTAGEMQEKIQNFAQ LPAHRVTDSC IVALIS 259
 QY 89 HGRBGFLEKGDENVKLENTPEALNNKQCALRAKPKVYIIOACRGQRDPG 140
 DB 260 HGVEGALYGVGKLLQLQEVFOLFNDNANCPSTLQNKPKMFFIOACRGDETDRG 311
 RESULT 15
 AAM26274
 ID AAM26274 standard; protein; 435 AA.
 AC AAM26274;
 XX
 DT 14-APR-1998 (first entry)
 XX
 DE Cell death protein ICH-1L.
 XX
 KW cell death; ICH-1L; interleukin-1 beta; apoptosis; treatment; IL-1;
 KW tumour; oncogenic transformation; IL-1 receptor antagonist; IL-1Ra;
 KW IL-1 beta.
 XX
 OS Homo sapiens.
 XX
 PN WO9733606-A1.
 XX
 PD 18-SEP-1997.
 XX
 PF 15-MAR-1996; 96WO-US003468.
 XX
 PR 15-MAR-1996; 96WO-US003468.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Yuan J, Friedlander R;
 XX WPI; 1997-470641/43.
 DR N-PSDB; AAT90565.
 XX
 PT Preventing apoptosis by blocking binding of interleukin-1beta to its
 PT receptor - useful for, e.g. treating tumours, and inhibiting oncogenic
 PT transformation.
 XX
 PS Example 5; Fig 7; 42pp; English.
 XX
 CC This is a cell death protein ICH-1L. The cell death caused by this ICH-1L
 CC can be prevented by a new method using IL-1 receptor antagonist (IL-1Ra).
 CC IL-1Ra is also used in a method for preventing programmed cell death by
 CC blocking the binding of interleukin-1 beta (IL-1 beta) to its receptor.
 CC Other methods for modulating programmed cell death are provided in the
 CC specification like a method of modulating apoptosis by activating the IL-

CC 1 beta converting enzyme (ICE) pathway and IL-1 beta production, a method
 CC for altering levels of hypoxia-induced cell death by blocking IL-1-
 CC mediated signal transduction, a method for killing oncogenically
 CC transformed cells by stimulating apoptosis with IL-1 beta or tumour
 CC necrosis factor alpha (TNF alpha), a method of inhibiting hypoxia-induced
 CC cell death by transfecting cells with the CrmA gene (of cowpox), and a
 CC method for modulating apoptosis by downregulating the IL-1 receptor. IL-
 CC 1Ra inhibits apoptosis induced by trophic factor depletion or hypoxia,
 CC while mature IL-1 beta induces cell death through a pathway independent
 CC of CrmA-sensitive gene activity, and cooperates with ICE and ICH-1L in
 CC apoptosis. Pro-IL-1 beta is the first substrate of any apoptosis-inducing
 CC gene. Increasing/decreasing cells death can be used for the treatment of
 CC tumours (or other conditions where apoptosis is involved). Altering cell
 CC death can also be used for inhibiting oncogenic transformation, and to
 CC treat complications involving apoptosis in cases of hypoxia or ischaemia.
 CC The methods can also be used to screen for agents that modulate
 CC apoptosis. When IL-1 beta is produced endogenously (via ICE) it mediates
 CC cell death, but when added exogenously it may stimulate death if it binds
 CC to its receptor after application of apoptotic stimulus or inhibit it by
 CC binding to the receptor before application of the stimulus
 CC
 XX
 SQ Sequence 435 AA;

Query Match 27.9%; Score 210; DB 2; Length 435;
 Best Local Similarity 37.5%; Pred. No. 8.6e-15;
 Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;
 QY 29 REGSEEDLDALHEMFRLRFESTMTKRDPTAEQFOEHLKEKFOQAIDSRDEPVSQAFVYVMA 68
 DB 202 RGGGDVDBHSTLVTLFRLGLGDAVAVLDCDQTAQEMQEKLNQFAQ-LPAHRYTDSQ-IVALLS 259
 QY 89 HAREGFLKGEDEGMVLEMLFEALNNKNCQALFAKPKVYIIOACRGEQRPDQ 140
 DB 260 HVEGALYGVGDGKLTLOEVEFQLFDNANCPSLQNKPKMFPIQACRGDETDTRG 311

Search completed: July 12, 2004, 13:47:47
 Job time : 44.438 secs

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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:45:17 ; Search time 12.6694 Seconds
(without alignments)
594.928 Million cell updates/sec

Title: US-10-068-564-5_COPY_1_146

Perfect score: 752
Sequence: 1 MSNPRSLSEKXYDMSGAAIA.....YIIQACRGQRDPGTWGD 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/iaa/PCITUS_COMB.pep:*
6: /cgn2_6/prodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	752	100.0	242	US-09-187-789-5	Sequence 5, Appli
2	747	99.3	230	US-09-187-789-7	Sequence 7, Appli
3	586	77.9	260	US-09-187-789-2	Sequence 2, Appli
4	586	77.9	260	US-09-139-600-2	Sequence 2, Appli
5	578	76.9	214	US-09-187-789-9	Sequence 9, Appli
6	293	39.0	74	US-09-187-789-63	Sequence 63, Appli
7	293	39.0	74	US-09-139-600-58	Sequence 58, Appli
8	210	27.9	421	US-08-983-502-10	Sequence 10, Appli
9	210	27.9	421	US-09-516-747-10	Sequence 10, Appli
10	210	27.9	421	PCT-US96-10521-10	Sequence 10, Appli
11	210	27.9	435	US-08-258-287B-53	Sequence 53, Appli
12	210	27.9	435	US-08-368-704C-51	Sequence 51, Appli
13	210	27.9	435	US-09-551-756-9	Sequence 9, Appli
14	210	27.9	435	US-09-227-721-9	Sequence 9, Appli
15	210	27.9	435	US-08-816-075-2	Sequence 2, Appli
16	210	27.9	435	US-08-724-378D-9	Sequence 9, Appli
17	210	27.9	435	US-09-954-697-9	Sequence 9, Appli
18	210	27.9	435	PCT-US94-07127A-4	Sequence 4, Appli
19	210	27.9	441	US-08-258-287B-44	Sequence 44, Appli
20	210	27.9	441	US-08-368-704C-43	Sequence 43, Appli
21	206	27.4	435	US-09-291-289-10	Sequence 10, Appli
22	197	26.2	312	US-08-258-287B-55	Sequence 55, Appli
23	197	26.2	312	US-08-368-704C-53	Sequence 53, Appli
24	190	25.3	56	US-09-187-789-64	Sequence 64, Appli
25	190	25.3	56	US-09-139-600-59	Sequence 59, Appli
26	189	25.1	404	US-09-445-724B-4	Sequence 4, Appli
27	189	25.1	404	US-09-445-724B-8	Sequence 8, Appli

28	187.5	24.9	311	2	US-08-391-916A-6	Sequence 6, Appli
29	187.5	24.9	383	2	US-08-391-916A-4	Sequence 4, Appli
30	187.5	24.9	404	1	US-08-203-716-2	Sequence 2, Appli
31	187.5	24.9	404	1	US-08-242-663A-2	Sequence 2, Appli
32	187.5	24.9	404	1	US-08-440-179-2	Sequence 2, Appli
33	187.5	24.9	404	2	US-08-450-130A-1	Sequence 1, Appli
34	187.5	24.9	404	2	US-08-391-916A-2	Sequence 2, Appli
35	187.5	24.9	404	2	US-08-573-890-2	Sequence 2, Appli
36	187.5	24.9	404	3	US-08-450-362A-1	Sequence 1, Appli
37	187.5	24.9	404	3	US-08-954-536-18	Sequence 18, Appli
38	187.5	24.9	404	3	US-09-039-657-2	Sequence 2, Appli
39	187.5	24.9	404	3	US-08-748-547-2	Sequence 2, Appli
40	187.5	24.9	404	3	US-08-908-436-3	Sequence 3, Appli
41	187.5	24.9	404	3	US-09-248-179-2	Sequence 2, Appli
42	187.5	24.9	404	4	US-09-069-023-30	Sequence 30, Appli
43	187.5	24.9	404	4	US-09-561-756-6	Sequence 6, Appli
44	187.5	24.9	404	4	US-09-227-721-6	Sequence 6, Appli
45	187.5	24.9	404	4	US-08-983-502-13	Sequence 13, Appli

ALIGNMENTS

RESULT 1
US-09-187-789-5
; Sequence 5, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emed S.
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-187-789-5

Query Match 100.0%; Score 752; DB 4; Length 242;
Best local similarity 100.0%; Pred. No. 3.5e-81; Mismatches 0; Gaps 0;
Matches 146; Conservative 0; Indels 0;
QY 1 MSNPRSLSEKXYDMSGAAIALILCVTKARGSEEDIDALEHFRQLRFESTMKRDPYAEQ 60
DB 1 MSNPRSLSEKXYDMSGAAIALILCVTKARGSEEDIDALEHFRQLRFESTMKRDPYAEQ 60
QY 61 FOEELKEFQALISREDPVSCAFVYLMHARGEGFLKGEDEMYKLEMLFEALNNKCOAL 120
DB 61 FOEELKEFQALISREDPVSCAFVYLMHARGEGFLKGEDEMYKLEMLFEALNNKCOAL 120
QY 121 RAKPKYIIQACRGQRDPGTWGD 146
DB 121 RAKPKYIIQACRGQRDPGTWGD 146
RESULT 2
US-09-187-789-7
; Sequence 7, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emed S.
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-187-789-7
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Query Match
Best Local Similarity 99.3%; Score 747; DB 4; Length 230;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MSNPRSLSEEEKYDMSGALALILCVTKARSGSEEDLDALEHMFROLRFESTMKRDPPTAEQ 60
DB 1 MSNPRSLSEEEKYDMSGALALILCVTKARSGSEEDLDALEHMFROLRFESTMKRDPPTAEQ 60
QY 61 FOEELKFOQALIDSRDPVSCAFVLMAGRGEGFLKGDGEMVYKLENTFEALNNKNCQAL 120
DB 61 FOEELKFOQALIDSRDPVSCAFVLMAGRGEGFLKGDGEMVYKLENTFEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGGEORDPGETVGGD 146
DB 121 RAKPKVYIIQACRGGEORDPGETVGGD 146
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RESULT 3
US-09-187-789-2
; Sequence 2, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-2
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Query Match
Best Local Similarity 77.9%; Score 586; DB 4; Length 260;
Matches 111; Conservative 18; Mismatches 17; Indels 0; Gaps 0;
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DB 8 MSNPRSLSEEEKYDMSGALALILCVTKARSGSEEDLDALEHMFROLRFESTMKRDPPTAEQ 67
QY 61 FOEELKFOQALIDSRDPVSCAFVLMAGRGEGFLKGDGEMVYKLENTFEALNNKNCQAL 120
DB 61 FOEELKFOQALIDSRDPVSCAFVLMAGRGEGFLKGDGEMVYKLENTFEALNNKNCQAL 127
QY 121 RAKPKVYIIQACRGGEORDPGETVGGD 146
DB 128 RAKPKVYIIQACRGGEORDPGETVGGD 153
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RESULT 4
US-09-139-600-2
; Sequence 2, Application US/09139600
; Patent No. 6432628
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434
; CURRENT APPLICATION NUMBER: US/09/139,600
; CURRENT FILING DATE: 1998-08-25
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; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-2
```

```
Query Match
Best Local Similarity 77.9%; Score 586; DB 4; Length 260;
Matches 111; Conservative 16; Mismatches 17; Indels 0; Gaps 0;
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QY 1 MSNPRSLSEEEKYDMSGALALILCVTKARSGSEEDLDALEHMFROLRFESTMKRDPPTAEQ 60
DB 8 MSNPRSLSEEEKYDMSGALALILCVTKARSGSEEDLDALEHMFROLRFESTMKRDPPTAEQ 67
QY 61 FOEELKFOQALIDSRDPVSCAFVLMAGRGEGFLKGDGEMVYKLENTFEALNNKNCQAL 120
DB 61 FOEELKFOQALIDSRDPVSCAFVLMAGRGEGFLKGDGEMVYKLENTFEALNNKNCQAL 127
QY 121 RAKPKVYIIQACRGGEORDPGETVGGD 146
DB 128 RAKPKVYIIQACRGGEORDPGETVGGD 153
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RESULT 5
US-09-187-789-9
; Sequence 9, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-187-789-9
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Query Match
Best Local Similarity 76.9%; Score 578; DB 4; Length 214;
Matches 117; Conservative 0; Mismatches 1; Indels 28; Gaps 1;
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DB 1 MSNPRSLSEEEKYDMSGALALILCVTKARSGSEEDLDALEHMFROLRFESTMKRDPPTAEQ 34
QY 61 FOEELKFOQALIDSRDPVSCAFVLMAGRGEGFLKGDGEMVYKLENTFEALNNKNCQAL 120
DB 35 FOEELKFOQALIDSRDPVSCAFVLMAGRGEGFLKGDGEMVYKLENTFEALNNKNCQAL 92
QY 121 RAKPKVYIIQACRGGEORDPGETVGGD 146
DB 93 RAKPKVYIIQACRGGEORDPGETVGGD 118
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RESULT 6
US-09-187-789-63
; Sequence 63, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
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COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,747
FILING DATE: 01-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/983,502
FILING DATE: <Unknown>
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-516-747-10

Query Match 27.9%; Score 210; DB 4; Length 421;
Best Local Similarity 37.5%; Pred. No. 1.8e-16;
Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;

QY 29 REGSEEDLALHEMFRLQREFTSTKRDPTABQFOEIELEKFOQAIDSRDPVSCAFVYVMA 88
DB 188 RSGGDVHSTLVTLFKLGDYVHLCQDTAQEMQEKLNPAQ-LPAHRYTDSCTVALLS 245
QY 89 HGREGFLEKGEDEGMVKLENLFEALNNKCOALPAKPKVYIIQACRGQRDPG 140
DB 246 HGEVGAIVGDGKLQLOEVFQLFDNANCPSLQNKPKMFIIQACRGQDETDRG 297

RESULT 10
PCT-US96-10521-10
Sequence 10, Application PC/TUS9610521
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
TITLE OF INVENTION: AND OTHER PROTEINS
NUMBER OF SEQUENCES: 34
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10521-10

Query Match 27.9%; Score 210; DB 5; Length 421;
Best Local Similarity 37.5%; Pred. No. 1.8e-16;
Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;

QY 29 REGSEEDLALHEMFRLQREFTSTKRDPTABQFOEIELEKFOQAIDSRDPVSCAFVYVMA 88
DB 188 RSGGDVHSTLVTLFKLGDYVHLCQDTAQEMQEKLNPAQ-LPAHRYTDSCTVALLS 245
QY 89 HGREGFLEKGEDEGMVKLENLFEALNNKCOALPAKPKVYIIQACRGQRDPG 140
DB 246 HGEVGAIVGDGKLQLOEVFQLFDNANCPSLQNKPKMFIIQACRGQDETDRG 297

RESULT 11
US-08-258-287B-53
Sequence 53, Application US/08258287B
Patent No. 6083735
GENERAL INFORMATION:
APPLICANT: Yuan, Junying
APPLICANT: Miura, Masayuki
TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,287B
FILING DATE: 10-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/080,850
FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609,3920001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-06-258-287B-53

Query Match 27.9%; Score 210; DB 3; Length 435;

Best Local Similarity 37.5%; Pred. No. 1.9e-16;
Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;

QY 29 REGSEEDLALHEMFQRLFEFTMKRDPFAEQFOEELKFOQALDSREDPVSCAFVYMA 88
DB 202 RSGGDVHSTLVTFLFKLGYDVHVLCDQTAQEMQEKLNFAQ-LPAHRYTDSCLVALLS 259

QY 89 HGRGFLKGEDEGVNKLFEALNNKNCQALRAKPKVYIIQACRGQRDPG 140
DB 260 HGVEGAIYGVGDKLLQLEVFQFLPDNANCPSLQNKPKMFFIQACRGDRTDRG 311

RESULT 12
US-08-368-704C-51
Sequence 51, Application US/08368704C
Patent No. 6087160

GENERAL INFORMATION:
APPLICANT: Yuan, Junying
APPLICANT: Maura, Masayuki
TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,704C
FILING DATE: 4-JAN-1995
CLASSIFICATION: 435
APPLICATION NUMBER: US 08/258,287
FILING DATE: 10-JUN-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/080,850
FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609,3920002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-368-704C-51

Query Match 27.9%; Score 210; DB 3; Length 435;
Best Local Similarity 37.5%; Pred. No. 1.9e-16;
Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;

QY 29 REGSEEDLALHEMFQRLFEFTMKRDPFAEQFOEELKFOQALDSREDPVSCAFVYMA 88
DB 202 RSGGDVHSTLVTFLFKLGYDVHVLCDQTAQEMQEKLNFAQ-LPAHRYTDSCLVALLS 259

QY 89 HGRGFLKGEDEGVNKLFEALNNKNCQALRAKPKVYIIQACRGQRDPG 140
DB 260 HGVEGAIYGVGDKLLQLEVFQFLPDNANCPSLQNKPKMFFIQACRGDRTDRG 311

RESULT 13
US-09-561-756-9
Sequence 9, Application US/09561756
Patent No. 6376226

GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
FILE REFERENCE: 480140,431
CURRENT APPLICATION NUMBER: US/09/561,756
CURRENT FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 09/227,721
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 435
TYPE: PRT
ORGANISM: Homo sapien
US-09-561-756-9

Query Match 27.9%; Score 210; DB 4; Length 435;
Best Local Similarity 37.5%; Pred. No. 1.9e-16;
Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;

QY 29 REGSEEDLALHEMFQRLFEFTMKRDPFAEQFOEELKFOQALDSREDPVSCAFVYMA 88
DB 202 RSGGDVHSTLVTFLFKLGYDVHVLCDQTAQEMQEKLNFAQ-LPAHRYTDSCLVALLS 259
QY 89 HGRGFLKGEDEGVNKLFEALNNKNCQALRAKPKVYIIQACRGQRDPG 140
DB 260 HGVEGAIYGVGDKLLQLEVFQFLPDNANCPSLQNKPKMFFIQACRGDRTDRG 311

RESULT 14
US-09-227-721-9
Sequence 9, Application US/09227721
Patent No. 6379950

GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
FILE REFERENCE: 480140,431
CURRENT APPLICATION NUMBER: US/09/227,721
CURRENT FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 435
TYPE: PRT
ORGANISM: Homo sapien
US-09-227-721-9

Query Match 27.9%; Score 210; DB 4; Length 435;
Best Local Similarity 37.5%; Pred. No. 1.9e-16;
Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;

QY 29 REGSEEDLALHEMFQRLFEFTMKRDPFAEQFOEELKFOQALDSREDPVSCAFVYMA 88
DB 202 RSGGDVHSTLVTFLFKLGYDVHVLCDQTAQEMQEKLNFAQ-LPAHRYTDSCLVALLS 259
QY 89 HGRGFLKGEDEGVNKLFEALNNKNCQALRAKPKVYIIQACRGQRDPG 140
DB 260 HGVEGAIYGVGDKLLQLEVFQFLPDNANCPSLQNKPKMFFIQACRGDRTDRG 311

RESULT 15

US-08-816-075-2
; Sequence 2, Application US/08816075
; Patent No. 6416753
; GENERAL INFORMATION:
; APPLICANT: Yuan, Junying
; APPLICANT: Friedlander, Robert
; TITLE OF INVENTION: Programmed Cell Death and Interleukin-1
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,075
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,524
; FILING DATE: 15-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0609,421001/JAG/LBB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-816-075-2

Query Match 27.9%; Score 210; DB 4; Length 435;
Best Local Similarity 37.5%; Pred. No. 1.9e-16;
Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;
QY 29 RRGSEEDLDALHEMFQRLRFESTMKRDPETAECFOEELKEKQQAIDSRDEPVSQAFVTLMA 88
Db 202 RSGGDVHDSTLVTLFELGIDVHVLCDQTAQEMOEKLNPAQ-LPAHRYTDSQ-IVALLS 259
QY 89 HGESEFLKSGDEGMVKLENLFEALNNKNCQALRAKPKVYLIQACRGEORDPG 140
Db 260 HGEVGAIVGVGKTLQLEVFQLEFDVANCPSLQNKPKMFPIQACRGDPTDRG 311

Search completed: July 12, 2004, 13:51:58
Job time : 13.6694 secs

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: July 12, 2004, 13:50:22 ; Search time 35.8967 Seconds
(without alignments)
1268.642 Million cell updates/sec

Title: US-10-068-564-5_COPY_1_146

Perfect score: 752
Sequence: 1 MSNPRSLSEKXDMGALAL.....YIIQACRGQRDPETVGGD 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1279676 seqs, 311918243 residues

Total number of hits satisfying chosen parameters: 1279676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/prodata/2/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/2/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/2/pubppa/PCTUS_PUBCOMB.pep.*
6: /cgn2_6/prodata/2/pubppa/US08_NEW_PUB.pep.*
7: /cgn2_6/prodata/2/pubppa/US08_PUBCOMB.pep.*
8: /cgn2_6/prodata/2/pubppa/US09_PUBCOMB.pep.*
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10: /cgn2_6/prodata/2/pubppa/US09_PUBCOMB.pep.*
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12: /cgn2_6/prodata/2/pubppa/US10_PUBCOMB.pep.*
13: /cgn2_6/prodata/2/pubppa/US10_PUBCOMB.pep.*
14: /cgn2_6/prodata/2/pubppa/US10_PUBCOMB.pep.*
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16: /cgn2_6/prodata/2/pubppa/US60_NEW_PUB.pep.*
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18: /cgn2_6/prodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	752	100.0	242	9 US-09-989-903-5	Sequence 5, Appl1
2	752	100.0	242	14 US-10-068-564-5	Sequence 5, Appl1
3	747	99.3	174	15 US-10-114-432-34	Sequence 34, Appl1
4	747	99.3	230	9 US-09-989-903-7	Sequence 7, Appl1
5	747	99.3	230	14 US-10-068-564-7	Sequence 7, Appl1
6	747	99.3	230	15 US-10-114-432-5	Sequence 15, Appl1
7	747	99.3	230	15 US-10-114-432-19	Sequence 19, Appl1
8	747	99.3	230	15 US-10-114-432-64	Sequence 64, Appl1
9	747	99.3	230	15 US-10-114-432-68	Sequence 68, Appl1
10	747	99.3	242	9 US-09-845-028-2	Sequence 2, Appl1
11	747	99.3	242	10 US-09-851-873-105	Sequence 105, Appl1
12	747	99.3	242	15 US-10-114-432-3	Sequence 3, Appl1
13	747	99.3	242	15 US-10-114-432-15	Sequence 15, Appl1
14	747	99.3	242	15 US-10-114-432-17	Sequence 17, Appl1
15	747	99.3	242	15 US-10-114-432-18	Sequence 18, Appl1

16	747	99.3	242	15 US-10-114-432-26	Sequence 26, Appl1
17	747	99.3	242	15 US-10-114-432-27	Sequence 27, Appl1
18	747	99.3	242	15 US-10-114-432-28	Sequence 28, Appl1
19	747	99.3	242	15 US-10-114-432-30	Sequence 30, Appl1
20	747	99.3	242	15 US-10-114-432-31	Sequence 31, Appl1
21	747	99.3	242	15 US-10-114-432-67	Sequence 67, Appl1
22	747	99.3	242	15 US-10-114-432-69	Sequence 69, Appl1
23	747	99.3	242	15 US-10-114-432-71	Sequence 71, Appl1
24	747	99.3	242	15 US-10-114-432-73	Sequence 73, Appl1
25	745	99.1	242	15 US-10-114-432-13	Sequence 13, Appl1
26	745	99.1	242	15 US-10-114-432-33	Sequence 33, Appl1
27	742	98.7	241	15 US-10-114-432-37	Sequence 37, Appl1
28	735	97.7	242	15 US-10-114-432-11	Sequence 11, Appl1
29	735	97.7	242	15 US-10-114-432-22	Sequence 22, Appl1
30	713	94.8	241	15 US-10-114-432-36	Sequence 36, Appl1
31	713	94.8	321	15 US-10-114-432-9	Sequence 9, Appl1
32	713	94.8	321	15 US-10-114-432-21	Sequence 21, Appl1
33	713	94.8	321	15 US-10-114-432-66	Sequence 66, Appl1
34	713	94.8	321	15 US-10-114-432-72	Sequence 72, Appl1
35	707	94.0	242	9 US-09-764-803A-24	Sequence 24, Appl1
36	702	93.4	242	9 US-09-845-028-9	Sequence 9, Appl1
37	681	90.6	134	15 US-10-114-432-32	Sequence 32, Appl1
38	681	90.6	134	15 US-10-114-432-33	Sequence 33, Appl1
39	681	90.6	146	15 US-10-114-432-7	Sequence 7, Appl1
40	681	90.6	146	15 US-10-114-432-20	Sequence 20, Appl1
41	681	90.6	146	15 US-10-114-432-65	Sequence 65, Appl1
42	681	90.6	146	15 US-10-114-432-70	Sequence 70, Appl1
43	679	90.3	229	9 US-09-764-803A-4	Sequence 4, Appl1
44	586	77.9	185	15 US-10-114-432-35	Sequence 35, Appl1
45	586	77.9	253	15 US-10-114-432-29	Sequence 29, Appl1

ALIGNMENTS

RESULT 1
US-09-989-903-5
; Sequence 5, Application US/09989903
; Patent No. US20020146804A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emdad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434D
; CURRENT APPLICATION NUMBER: US/09/989,903
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-989-903-5

Query Match 100.0%; Score 752; DB 9; Length 242;

Best Local Similarity 100.0%; Pred. No. 2.2e-70; Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSNPRSLSEKXDMGALALILCVTKARSGSEEDLDALSHNRQRLRFESTMKDPTAAQ	60
DB	1	MSNPRSLSEKXDMGALALILCVTKARSGSEEDLDALSHNRQRLRFESTMKDPTAAQ	60
QY	61	FOEELKFKQALDSREDPVSCAFVYLMAGHBEGLKEDGEMVYLENLFELANKNCAL	120
DB	61	FOEELKFKQALDSREDPVSCAFVYLMAGHBEGLKEDGEMVYLENLFELANKNCAL	120
QY	121	RKPKVYIIQACRGQRDPETVGGD	146
DB	121	RKPKVYIIQACRGQRDPETVGGD	146

RESULT 2

US-10-068-564-5
; Sequence 5, Application US/10068564
; Publication No. US20030040096A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emdad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C2
; CURRENT APPLICATION NUMBER: US/10/068,564
; CURRENT FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 242
; TYPE: PRN
; ORGANISM: Homo sapien
US-10-068-564-5

Query Match 100.0%; Score 752; DB 14; Length 242;
Best Local Similarity 100.0%; Pred. No. 2.2e-70;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSNPSLEEEKYDMSGALALILCVTKAREGSEEDLDALHMFROLPFESTMKRDPPTAEQ 60
DB 1 MSNPSLEEEKYDMSGALALILCVTKAREGSEEDLDALHMFROLPFESTMKRDPPTAEQ 60
QY 61 FOEELKFOQAIDSRDPVSCAFVILMAHGREGFLKGEDGEMVKLENLFEALNNKCOAL 120
DB 61 FOEELKFOQAIDSRDPVSCAFVILMAHGREGFLKGEDGEMVKLENLFEALNNKCOAL 120
QY 121 RAKPKVYIIQACRGQRDPGETVGGD 146
DB 121 RAKPKVYIIQACRGQRDPGETVGGD 146

RESULT 3
US-10-114-432-34
; Sequence 34, Application US/10114432
; Publication No. US2004001915A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobiwits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P1F1 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 174
; TYPE: PRN
; ORGANISM: Homo Sapiens
US-10-114-432-34

Query Match 99.3%; Score 747; DB 15; Length 174;
Best Local Similarity 99.3%; Pred. No. 4.7e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPSLEEEKYDMSGALALILCVTKAREGSEEDLDALHMFROLPFESTMKRDPPTAEQ 60
DB 1 MSNPSLEEEKYDMSGALALILCVTKAREGSEEDLDALHMFROLPFESTMKRDPPTAEQ 60
QY 61 FOEELKFOQAIDSRDPVSCAFVILMAHGREGFLKGEDGEMVKLENLFEALNNKCOAL 120
DB 61 FOEELKFOQAIDSRDPVSCAFVILMAHGREGFLKGEDGEMVKLENLFEALNNKCOAL 120

QY 121 RAKPKVYIIQACRGQRDPGETVGGD 146
DB 121 RAKPKVYIIQACRGQRDPGETVGGD 146

RESULT 4
US-09-989-903-7
; Sequence 7, Application US/09989903
; Patent No. US20020146804A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emdad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434D1
; CURRENT APPLICATION NUMBER: US/09/989,903
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 230
; TYPE: PRN
; ORGANISM: Homo sapien
US-09-989-903-7

Query Match 99.3%; Score 747; DB 9; Length 230;
Best Local Similarity 99.3%; Pred. No. 6.8e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPSLEEEKYDMSGALALILCVTKAREGSEEDLDALHMFROLPFESTMKRDPPTAEQ 60
DB 1 MSNPSLEEEKYDMSGALALILCVTKAREGSEEDLDALHMFROLPFESTMKRDPPTAEQ 60
QY 61 FOEELKFOQAIDSRDPVSCAFVILMAHGREGFLKGEDGEMVKLENLFEALNNKCOAL 120
DB 61 FOEELKFOQAIDSRDPVSCAFVILMAHGREGFLKGEDGEMVKLENLFEALNNKCOAL 120
QY 121 RAKPKVYIIQACRGQRDPGETVGGD 146
DB 121 RAKPKVYIIQACRGQRDPGETVGGD 146

RESULT 5
US-10-068-564-7
; Sequence 7, Application US/10068564
; Publication No. US20030040096A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emdad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C2
; CURRENT APPLICATION NUMBER: US/10/068,564
; CURRENT FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 230
; TYPE: PRN
; ORGANISM: Homo sapien
US-10-068-564-7

Query Match 99.3%; Score 747; DB 14; Length 230;
Best Local Similarity 99.3%; Pred. No. 6.8e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPSLEEEKYDMSGALALILCVTKAREGSEEDLDALHMFROLPFESTMKRDPPTAEQ 60
DB 1 MSNPSLEEEKYDMSGALALILCVTKAREGSEEDLDALHMFROLPFESTMKRDPPTAEQ 60
QY 61 FOEELKFOQAIDSRDPVSCAFVILMAHGREGFLKGEDGEMVKLENLFEALNNKCOAL 120
DB 61 FOEELKFOQAIDSRDPVSCAFVILMAHGREGFLKGEDGEMVKLENLFEALNNKCOAL 120

Db 61 FOEIELEKFOQAIDSREDPVSCAFVYLMHGREBGLKGEDGEMVKLENLFEALNNKCOAL 120

QY 121 RAKPKVYIIQACRGGEQRPGETVGD 146

Db 121 RAKPKVYIIQACRGGEQRPGETVGD 146

RESULT 6
US-10-114-432-5
; Sequence 5, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P1I1 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-5

Query Match 99.3%; Score 747; DB 15; Length 230;
Best Local Similarity 99.3%; Pred. No. 6.8e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLEBEKYMGSALALILCVTKARBSBEDDLEHMRQRLFESTMKRDPTAEQ 60

Db 1 MSNPRSLEBEKYMGSARLALILCVTKARBSBEDDLEHMRQRLFESTMKRDPTAEQ 60

QY 61 FOEIELEKFOQAIDSREDPVSCAFVYLMHGREBGLKGEDGEMVKLENLFEALNNKCOAL 120

Db 61 FOEIELEKFOQAIDSREDPVSCAFVYLMHGREBGLKGEDGEMVKLENLFEALNNKCOAL 120

QY 121 RAKPKVYIIQACRGGEQRPGETVGD 146

Db 121 RAKPKVYIIQACRGGEQRPGETVGD 146

RESULT 7
US-10-114-432-19
; Sequence 19, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P1I1 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 230
; TYPE: PRT

; ORGANISM: Homo Sapiens
US-10-114-432-19

Query Match 99.3%; Score 747; DB 15; Length 230;
Best Local Similarity 99.3%; Pred. No. 6.8e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLEBEKYMGSALALILCVTKARBSBEDDLEHMRQRLFESTMKRDPTAEQ 60

Db 1 MSNPRSLEBEKYMGSARLALILCVTKARBSBEDDLEHMRQRLFESTMKRDPTAEQ 60

QY 61 FOEIELEKFOQAIDSREDPVSCAFVYLMHGREBGLKGEDGEMVKLENLFEALNNKCOAL 120

Db 61 FOEIELEKFOQAIDSREDPVSCAFVYLMHGREBGLKGEDGEMVKLENLFEALNNKCOAL 120

QY 121 RAKPKVYIIQACRGGEQRPGETVGD 146

Db 121 RAKPKVYIIQACRGGEQRPGETVGD 146

RESULT 8
US-10-114-432-64
; Sequence 64, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P1I1 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-64

Query Match 99.3%; Score 747; DB 15; Length 230;
Best Local Similarity 99.3%; Pred. No. 6.8e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLEBEKYMGSALALILCVTKARBSBEDDLEHMRQRLFESTMKRDPTAEQ 60

Db 1 MSNPRSLEBEKYMGSARLALILCVTKARBSBEDDLEHMRQRLFESTMKRDPTAEQ 60

QY 61 FOEIELEKFOQAIDSREDPVSCAFVYLMHGREBGLKGEDGEMVKLENLFEALNNKCOAL 120

Db 61 FOEIELEKFOQAIDSREDPVSCAFVYLMHGREBGLKGEDGEMVKLENLFEALNNKCOAL 120

QY 121 RAKPKVYIIQACRGGEQRPGETVGD 146

Db 121 RAKPKVYIIQACRGGEQRPGETVGD 146

RESULT 9
US-10-114-432-68
; Sequence 68, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.

```

; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P1.F11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114.432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-68
```

```

Query Match          99.3%; Score 747; DB 15; Length 230;
Best Local Similarity 99.3%; Pred. No. 6.8e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MSNPRSLSEEEKYDMSGALALILCVTKARBSSEEDLDALHEMFROLRFESTMKRDPPTAQ 60
DB 1 MSNPRSLSEEEKYDMSGARLALILCVTKARBSSEEDLDALHEMFROLRFESTMKRDPPTAQ 60
QY 61 FOEBLEKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
DB 61 FOEBLEKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGQRDPGETVGGD 146
DB 121 RAKPKVYIIQACRGQRDPGETVGGD 146
```

```

RESULT 10
US-09-845-028-2
; Sequence 2, Application US/09845028
; Patent No. US20020081705A1
; GENERAL INFORMATION:
; APPLICANT: Mankovich, John
; TITLE OF INVENTION: HUMAN CASPASE-14 COMPOSITIONS
; FILE REFERENCE: BBI-111
; CURRENT APPLICATION NUMBER: US/09/845,028
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/199,962
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-028-2
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```

Query Match          99.3%; Score 747; DB 9; Length 242;
Best Local Similarity 99.3%; Pred. No. 7.3e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```

QY 1 MSNPRSLSEEEKYDMSGALALILCVTKARBSSEEDLDALHEMFROLRFESTMKRDPPTAQ 60
DB 1 MSNPRSLSEEEKYDMSGARLALILCVTKARBSSEEDLDALHEMFROLRFESTMKRDPPTAQ 60
QY 61 FOEBLEKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
DB 61 FOEBLEKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGQRDPGETVGGD 146
DB 121 RAKPKVYIIQACRGQRDPGETVGGD 146
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```

RESULT 11
US-09-851-873-105
; Sequence 105, Application US/09851873
```

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; Publication No. US20030165488A1
; GENERAL INFORMATION:
; APPLICANT: Klezlien, Rolf F
; APPLICANT: Reardon, Ilene M
; APPLICANT: Weiland, Katherine L
; TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
; FILE REFERENCE: 28341/0023
; CURRENT APPLICATION NUMBER: US/09/851,873
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-873-105
```

```

Query Match          99.3%; Score 747; DB 10; Length 242;
Best Local Similarity 99.3%; Pred. No. 7.3e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```

QY 1 MSNPRSLSEEEKYDMSGALALILCVTKARBSSEEDLDALHEMFROLRFESTMKRDPPTAQ 60
DB 1 MSNPRSLSEEEKYDMSGARLALILCVTKARBSSEEDLDALHEMFROLRFESTMKRDPPTAQ 60
QY 61 FOEBLEKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
DB 61 FOEBLEKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGQRDPGETVGGD 146
DB 121 RAKPKVYIIQACRGQRDPGETVGGD 146
```

```

RESULT 12
US-10-114-432-3
; Sequence 3, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P1.F11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-3
```

```

Query Match          99.3%; Score 747; DB 15; Length 242;
Best Local Similarity 99.3%; Pred. No. 7.3e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 1 MSNPRSLSEEEKYDMSGALALILCVTKARBSSEEDLDALHEMFROLRFESTMKRDPPTAQ 60
DB 1 MSNPRSLSEEEKYDMSGARLALILCVTKARBSSEEDLDALHEMFROLRFESTMKRDPPTAQ 60
QY 61 FOEBLEKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
DB 61 FOEBLEKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGQRDPGETVGGD 146
```

DB 121 RAKPKYIIIOACRGEORDPGETVGD 146

RESULT 13

US-10-114-432-15
; Sequence 15, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Mangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-15

Query Match 99.3%; Score 747; DB 15; Length 242;
Best Local Similarity 99.3%; Pred. No. 7.3e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRLSEEEKYMSGAALAILCVTKARSGSEEDLDALHMFROLRFESTMKRDPYAEQ 60
DB 1 MSNPRLSEEEKYMSGAALAILCVTKARSGSEEDLDALHMFROLRFESTMKRDPYAEQ 60
QY 61 FOELEKFOQAIDSREDPVSCAFVVLMAHGRBGLKGEDEMYKLENTFALNNKCOAL 120
DB 61 FOELEKFOQAIDSREDPVSCAFVVLMAHGRBGLKGEDEMYKLENTFALNNKCOAL 120

QY 121 RAKPKYIIIOACRGEORDPGETVGD 146
DB 121 RAKPKYIIIOACRGEORDPGETVGD 146

RESULT 14

US-10-114-432-17
; Sequence 17, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Mangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-17

Query Match 99.3%; Score 747; DB 15; Length 242;
Best Local Similarity 99.3%; Pred. No. 7.3e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRLSEEEKYMSGAALAILCVTKARSGSEEDLDALHMFROLRFESTMKRDPYAEQ 60
DB 1 MSNPRLSEEEKYMSGAALAILCVTKARSGSEEDLDALHMFROLRFESTMKRDPYAEQ 60
QY 61 FOELEKFOQAIDSREDPVSCAFVVLMAHGRBGLKGEDEMYKLENTFALNNKCOAL 120
DB 61 FOELEKFOQAIDSREDPVSCAFVVLMAHGRBGLKGEDEMYKLENTFALNNKCOAL 120
QY 121 RAKPKYIIIOACRGEORDPGETVGD 146
DB 121 RAKPKYIIIOACRGEORDPGETVGD 146

RESULT 15

US-10-114-432-18
; Sequence 18, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Mangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-18

Query Match 99.3%; Score 747; DB 15; Length 242;
Best Local Similarity 99.3%; Pred. No. 7.3e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRLSEEEKYMSGAALAILCVTKARSGSEEDLDALHMFROLRFESTMKRDPYAEQ 60
DB 1 MSNPRLSEEEKYMSGAALAILCVTKARSGSEEDLDALHMFROLRFESTMKRDPYAEQ 60
QY 61 FOELEKFOQAIDSREDPVSCAFVVLMAHGRBGLKGEDEMYKLENTFALNNKCOAL 120
DB 61 FOELEKFOQAIDSREDPVSCAFVVLMAHGRBGLKGEDEMYKLENTFALNNKCOAL 120
QY 121 RAKPKYIIIOACRGEORDPGETVGD 146
DB 121 RAKPKYIIIOACRGEORDPGETVGD 146

Search completed: July 12, 2004, 14:04:00
Job time : 35.8967 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:44:06 ; Search time 10.5579 Seconds
(without alignments)
1330.191 Million cell updates/sec

Title: US-10-068-564-5_COPY_1_146

Perfect score: 752
Sequence: 1 MSNPRSLSEKXYDMSGALIA.....YIIQACRGEQRPGETVGGD 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	747	99.3	242	2 JC7517	caspase-14/a - hum
2	210	27.9	435	2 A54821	apoptosis regulato
3	205	27.3	182	2 I67436	interleukin-1-beta
4	205	27.3	452	2 JC6507	caspase-2 - rat
5	197	26.2	312	2 B54821	apoptosis regulato
6	194	25.8	454	2 JC7123	caspase-9 long cha
7	187.5	24.9	311	2 B56084	interleukin-1beta
8	187.5	24.9	383	2 A56084	interleukin-1beta
9	187.5	24.9	404	2 A42677	interleukin-1beta
10	185.5	24.7	263	2 C56084	interleukin-1beta
11	179.5	23.9	277	2 A55315	cysteine proteinas
12	175	23.3	418	2 B57511	interleukin-1 beta
13	174.5	23.2	212	2 I67437	cysteine proteinas
14	173	23.0	402	2 A46495	IF-1 beta converta
15	171.5	22.8	277	2 JC5410	CPP32 protein - mo
16	168.5	22.4	377	2 B64710	cysteine proteinas
17	168	22.3	377	2 A57511	interleukin-1 beta
18	167	22.2	416	2 G02635	ICE-LAP6 - human
19	151	20.1	495	2 T20038	hypothetical prote
20	151	20.1	503	2 A49429	interleukin-1 beta
21	132	17.6	826	2 T43638	caspase-related pr
22	127.5	17.0	136	2 I53300	interleukin-1-beta
23	94.5	12.6	536	2 T43637	caspase-related pr
24	92	12.2	1313	2 A48467	myosin heavy chain
25	89.5	11.9	642	2 T27021	hypothetical prote
26	88.5	11.8	149	2 T43637	caspase protein 1C
27	84.5	11.2	520	2 F70350	recombination prot
28	82.5	11.0	167	2 S70824	hypothetical prote
29	82	10.9	1957	2 A45627	myosin heavy chain

30	81.5	10.8	484	2 F81859	conserved hypothet
31	81.5	10.8	484	2 F81083	conserved hypothet
32	79	10.5	676	2 S00084	myosin heavy chain
33	79	10.5	918	2 C96829	unknown protein F1
34	79	10.5	1957	2 A59294	skeletal myosin -
35	78	10.4	510	2 S42626	ER-golgi intermedi
36	78	10.4	1389	2 T41230	hypothetical TPR d
37	77	10.2	354	2 B75003	hypothetical prote
38	77	10.2	599	2 G83941	ABC transporter (A
39	77	10.2	906	2 G69531	alanyl-tRNA synthet
40	77	10.2	1225	2 A56514	chromokinesin - ch
41	77	10.2	1265	2 T07397	kinasin heavy chain
42	76.5	10.2	415	2 S35760	fcra protein precu
43	76.5	10.2	468	2 TWMSE2	transcription fact
44	76	10.1	154	2 B81866	conserved hypothet
45	76	10.1	627	2 A69663	DNA mismatch repai

ALIGNMENTS

RESULT 1

JC7517

C:Species: Homo sapiens (man)

C>Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

C/Accession: JC7517

R/Eckhart, L.; Ban, J.; Fischer, H.; Tschachler, E.

Biochem. Biophys. Res. Commun. 277, 655-659, 2000

A>Title: Caspase-14: Analysis of gene structure and mRNA expression during keratinocyte

A/Reference number: JC7517; MUID:20517231; PMID:11062009

A/Contents: Epidermal keratinocytes

A/Accession: JC7517

A/Molecule type: mRNA

A/Residues: 1-242 <ECK>

A/Cross-references: GB:AF097874

C/Comment: This enzyme accumulates during keratinocyte differentiation and is activate

A/Map position: 19p13.1

A/Introns: 9/3; 59/3; 135/1; 174/1; 208/3

C/Keywords: differentiation

Query Match	Score	DB 2:	Length
Best Local Similarity	99.3%	Pred. No. 1.1e-57;	242;
Matches 145; Conservative	0;	Mismatches 1;	Gaps 0;
QY	1	MSNPRSLSEKXYDMSGALIALILCTKARSGSEDDIDALHMFROLFESTMKRDPPTAQ	60
DB	1	MSNPRSLSEKXYDMSGARLILCTKARSGSEDDIDALHMFROLFESTMKRDPPTAQ	60
QY	61	FOELEKFOQALDSREDPVSCAFVIMAHGRBGLKGEDEMYKLEMLFEALNNKCOAL	120
DB	61	FOELEKFOQALDSREDPVSCAFVIMAHGRBGLKGEDEMYKLEMLFEALNNKCOAL	120
QY	121	RAKPKYIIQACRGEQRPGETVGGD	146
DB	121	RAKPKYIIQACRGEQRPGETVGGD	146

RESULT 2

A54821

C:Species: Homo sapiens (man)

C/Accession: A54821

R/Mang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.

Cell 78, 739-750, 1994

A>Title: Ich-1, an Ice/ced-3-related gene, encodes both positive and negative regulato

A/Reference number: A54821; MUID:94373811; PMID:8087842

A/Accession: A54821

A/Status: preliminary

A/Molecule type: mRNA

A;Residues: 1-435 <MAN>
A;Cross-references: GB:U13021; NID:9537291; PID:9537292
C;Keywords: alternative splicing; apoptosis

Query Match 27.9%; Score 210; DB 2; Length 435;
Best Local Similarity 37.5%; Pred. No. 9.4e-11;
Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;

QY 29 REGSEEDLDALHMFROLFEFTMKRDPPTAEOFOEELKFOQAIDSREDPVSCAFVYMA 88
Db 202 RSGGDVHSTLVTLVTLFKLIGVNVHVCDDTAQEMOEKIQNPAQ-LPAHRTDSC-IVALIS 259
QY 89 HGRGFLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGGEQDPG 140
Db 260 HGVGALTYGVGDKLQLQEVFQLFDNANCPSLQNKPKMFFIQACRGDETDG 311

RESULT 3

167436
interleukin-1-beta-converting enzyme and ced-3 homolog-1, long isoform - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: 167436
R;Flaws: J.A.; Kugu, K.; Tshovich, A.M.; Desanti, A.; Tilly, K.I.; Hirschfeld, A.N.; Tili
Endocrinology 136; 5042-5053, 1995
A;Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cel
nuloa cells of the ovarian follicle.
A;Reference number: 153300; PMID:96042508; PMID:7586240
A;Accession: 167436
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-182 <RSS>
A;Cross-references: EMBL:U34684; NID:g1004368; PID:AA52260.1; PID:g1004369

Query Match 27.3%; Score 205; DB 2; Length 182;
Best Local Similarity 37.5%; Pred. No. 9.6e-11;
Matches 42; Conservative 27; Mismatches 41; Indels 2; Gaps 2;

QY 29 REGSEEDLDALHMFROLFEFTMKRDPPTAEOFOEELKFOQAIDSREDPVSCAFVYMA 88
Db 22 RSGGDVHSTLVTLVTLFKLIGVNVHVCDDTAQEMOEKIQNPAQ-LPAHRTDSC-IVALIS 79
QY 89 HGRGFLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGGEQDPG 140
Db 80 HGVGALTYGVGDKLQLQEVFQLFDNANCPSLQNKPKMFFIQACRGDETDG 131

RESULT 4

JC6507
Caspase-2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: JC6507
R;Sato, N.; Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.
Gene 202; 121-132, 1997
A;Title: Cloning and expression of the cDNA encoding rat caspase-2.
A;Reference number: JC6507; PMID:98087427; PMID:9427555
A;Accession: JC6507
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-452 <SAT>
A;Cross-references: GB:U77933; NID:g2769705; PID:AA596379.1; PID:g2769706

Query Match 27.3%; Score 205; DB 2; Length 452;
Best Local Similarity 37.5%; Pred. No. 2.7e-10;
Matches 42; Conservative 27; Mismatches 41; Indels 2; Gaps 2;

QY 29 REGSEEDLDALHMFROLFEFTMKRDPPTAEOFOEELKFOQAIDSREDPVSCAFVYMA 88
Db 219 RSGGDVHSTLVTLVTLFKLIGVNVHVCDDTAQEMOEKIQNPAQ-LPAHRTDSC-IVALIS 276
QY 89 HGRGFLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGGEQDPG 140

Db 277 HGVGALTYGVGDKLQLQEVFQLFDNANCPSLQNKPKMFFIQACRGDETDG 328

RESULT 5

B54821
apoptosis regulator ICH-1, suppressive form S - human
C;Species: Homo sapiens (man)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
C;Accession: B54821
R;Wang, L.; Mura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
Cell 78; 739-750, 1994
A;Title: Ich-1, an Ice/ced-3-related gene, encodes both positive and negative regulator.
A;Reference number: B54821; PMID:94373811; PMID:8087842
A;Accession: B54821
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-312 <MAN>
A;Cross-references: GB:U10322
C;Keywords: alternative splicing; apoptosis

Query Match 26.2%; Score 197; DB 2; Length 312;
Best Local Similarity 37.7%; Pred. No. 8.7e-10;
Matches 40; Conservative 27; Mismatches 37; Indels 2; Gaps 2;

QY 29 REGSEEDLDALHMFROLFEFTMKRDPPTAEOFOEELKFOQAIDSREDPVSCAFVYMA 88
Db 188 RSGGDVHSTLVTLVTLFKLIGVNVHVCDDTAQEMOEKIQNPAQ-LPAHRTDSC-IVALIS 245
QY 89 HGRGFLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRG 134
Db 246 HGVGALTYGVGDKLQLQEVFQLFDNANCPSLQNKPKMFFIQACRG 291

RESULT 6

JC7123
caspase-9 long chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C;Accession: JC7123
R;Fujiwara, E.; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikawa, U.; Momoi, T.
Biochem. Biophys. Res. Commun. 264; 550-555, 1999
A;Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9.
A;Reference number: JC7123; PMID:20001956; PMID:10529400
A;Accession: JC7123
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-454 <FUY>
A;Cross-references: DBJ:AB019600; NID:g6440941; PID:g6440942

Query Match 25.8%; Score 194; DB 2; Length 454;
Best Local Similarity 37.4%; Pred. No. 2.4e-09;
Matches 46; Conservative 17; Mismatches 42; Indels 18; Gaps 3;

QY 29 REGSEEDLDALHMFROLFEFTMKRDPPTAEOFOEELKFOQAIDSREDPVSCAFV 84
Db 218 RSGSNIDRKLHRRFRLMFPVYVKNLDTAKKQVTAALMAHNRHALD-----CFVY 270
QY 85 VIMAGRE-----GFLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRG 137
Db 271 VILSHGQASHLQFGAVYGTGCSVSIKIVNFNGSGCPSLGGKPKLFFIQACGGEQK 330
QY 138 DPG 140
Db 331 DHG 333

RESULT 7

B56084
interleukin-1beta converting enzyme gamma isozyyme - human
C;Species: Homo sapiens (man)
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
C;Accession: B56084
R;Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.

J. Biol. Chem. 270, 4312-4317, 1995
 A>Title: Cloning and expression of four novel isoforms of human interleukin-1beta converting enzyme
 A:Reference number: A56084; MUID:95181414; PMID:7876192
 A:Accession: B56084
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-311 <ALN>
 A:Cross-references: GB:U13698; NID:9717041; PIDN:AAC50108.1; PID:9717042
 C:Genetics:
 A:Gene: IL1BCE
 C:Keywords: alternative splicing

Query Match 24.9%; Score 187.5; DB 2; Length 311;
 Best Local Similarity 35.2%; Pred. No. 5.8e-09;
 Matches 51; Conservative 23; Mismatches 52; Indels 19; Gaps 6;

QY 15 SGAAALILCVTK-----AREGSEEDLDLEHMFRLPFSITMKRDPPTAQQFOEELKFKQ 69
 DB 67 SRTRLALITCNEEFDSIPRTGAEVDITGWTMLQNGYSVDVKKULTASDMTELEAFA 126
 QY 70 QAIDSEDPVSCAFVYLMAHG-REGFLKGEDEGVN---KLENLFEALNNKNCQALRAKP 124
 DB 127 HREPHKTS--DSTFLVFMHSGIRREGICGKHSEQVDPDIQLNMAIFNMLTKNCPSLKDKP 184
 QY 125 KVTITQACRGEQRPDQ-----ETVG 144
 DB 185 KVTITQACRGD--SPGVVWFKDSVG 207

RESULT 8
 A56084
 interleukin-1beta converting enzyme beta isozyme - human
 C:Species: Homo sapiens (man)
 C>Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
 C:Accession: A56084
 R:Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
 J. Biol. Chem. 270, 4312-4317, 1995
 A>Title: Cloning and expression of four novel isoforms of human interleukin-1beta conver
 A:Reference number: A56084; MUID:95181414; PMID:7876192
 A:Accession: A56084
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-383 <ALN>
 A:Cross-references: GB:U13697; NID:9717039; PIDN:AAC50107.1; PID:9717040
 C:Genetics:
 A:Gene: IL1BCE
 C:Keywords: alternative splicing

Query Match 24.9%; Score 187.5; DB 2; Length 383;
 Best Local Similarity 35.2%; Pred. No. 7.3e-09;
 Matches 51; Conservative 23; Mismatches 52; Indels 19; Gaps 6;

QY 15 SGAAALILCVTK-----AREGSEEDLDLEHMFRLPFSITMKRDPPTAQQFOEELKFKQ 69
 DB 139 SRTRLALITCNEEFDSIPRTGAEVDITGWTMLQNGYSVDVKKULTASDMTELEAFA 198
 QY 70 QAIDSEDPVSCAFVYLMAHG-REGFLKGEDEGVN---KLENLFEALNNKNCQALRAKP 124
 DB 199 HREPHKTS--DSTFLVFMHSGIRREGICGKHSEQVDPDIQLNMAIFNMLTKNCPSLKDKP 256
 QY 125 KVTITQACRGEQRPDQ-----ETVG 144
 DB 257 KVTITQACRGD--SPGVVWFKDSVG 279

RESULT 9
 A42677
 interleukin-1 beta converting enzyme (EC 3.4.22.-) - human
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
 C:Accession: A54263; A42677; S21734; S24164
 R:Cerretti, D.P.; Hollingsworth, L.T.; Kozlosky, C.J.; Valentine, M.B.; Shapiro, D.N.; M
 Genomics 20, 468-473, 1994

A>Title: Molecular characterization of the gene for human interleukin-1beta converting
 A:Reference number: A54263; MUID:94307734; PMID:8034320
 A:Accession: A54263
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-404 <CE2>
 A:Cross-references: GB:L27475
 R:Cerretti, D.P.; Kozlosky, C.J.; Mosley, B.; Nelson, N.; Van Ness, K.; Greenstreet, T
 Science 256, 97-100, 1992
 A>Title: Molecular cloning of the interleukin-1beta converting enzyme.
 A:Reference number: A42677; MUID:92229430; PMID:1373520
 A:Accession: A42677
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-404 <CE>
 A:Cross-references: GB:M87507; NID:9435598; PIDN:AAA66942.1; PID:9186286
 R:Chomberg, N.A.; Bull, H.G.; Calaycay, J.R.; Chapman, K.T.; Howard, A.D.; Kostura, N
 J.; Ding, G.C.F.; Egger, L.A.; Gaffney, E.P.; Limuoco, G.; Palyha, O.C.; Raju, S.M.; R
 cci, M.J.
 Nature 356, 768-774, 1992
 A>Title: A novel heterodimeric cysteine protease is required for interleukin-1beta pro
 A:Reference number: S21734; MUID:92244338; PMID:1574116
 A:Accession: S21734
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-404 <THO>
 A:Cross-references: EMBL:X65019; NID:933792; PIDN:CAA46153.1; PID:933793
 R:Kronheim, S.R.; Muma, A.; Greenstreet, T.; Glackin, P.J.; van Ness, K.; March, C.J.
 Arch. Biochem. Biophys. 296, 698-703, 1992
 A>Title: Purification of interleukin-1beta converting enzyme, the protease that cleave
 A:Reference number: S24164; MUID:92337439; PMID:1321594
 A:Accession: S24164
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 120-135, 'AX', 138-139, 'X', 141-142 <KRO>
 A:Gene: GDB:IL1BC
 A:Cross-references: GDB:132368; OMIM:147678
 A:Map position: 11q23-11q23
 C:Keywords: cysteine proteinase; hydrolase

Query Match 24.9%; Score 187.5; DB 2; Length 404;
 Best Local Similarity 35.2%; Pred. No. 7.8e-09;
 Matches 51; Conservative 23; Mismatches 52; Indels 19; Gaps 6;

QY 15 SGAAALILCVTK-----AREGSEEDLDLEHMFRLPFSITMKRDPPTAQQFOEELKFKQ 69
 DB 160 SRTRLALITCNEEFDSIPRTGAEVDITGWTMLQNGYSVDVKKULTASDMTELEAFA 219
 QY 70 QAIDSEDPVSCAFVYLMAHG-REGFLKGEDEGVN---KLENLFEALNNKNCQALRAKP 124
 DB 220 HREPHKTS--DSTFLVFMHSGIRREGICGKHSEQVDPDIQLNMAIFNMLTKNCPSLKDKP 277
 QY 125 KVTITQACRGEQRPDQ-----ETVG 144
 DB 278 KVTITQACRGD--SPGVVWFKDSVG 300

RESULT 10
 C56084
 interleukin-1beta converting enzyme delta isozyme - human
 C:Species: Homo sapiens (man)
 C>Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
 C:Accession: C56084
 R:Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
 J. Biol. Chem. 270, 4312-4317, 1995
 A>Title: Cloning and expression of four novel isoforms of human interleukin-1beta conv
 A:Reference number: A56084; MUID:95181414; PMID:7876192
 A:Accession: C56084
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-263 <ALN>
 A:Cross-references: GB:U13699; NID:9717043; PIDN:AAC50109.1; PID:9717044

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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:40:11 ; Search time 7.23967 Seconds

(without alignments)
1050.081 Million cell updates/sec

Title: US-10-068-564-5_COPY_1_146

Perfect score: 752
Sequence: 1 MSNPRSEEEKYDMSGALA.....YIQACRGQRDPGETVGAD 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	747	99.3	242	1	ICB6_HUMAN
2	586	77.9	257	1	ICB6_MOUSE
3	222	29.5	424	1	ICB2_CHICK
4	210	27.9	435	1	ICB2_HUMAN
5	207	27.5	435	1	ICB2_MOUSE
6	205	27.3	312	1	ICB2_RAT
7	187.5	24.9	404	1	ICB6_HUMAN
8	184	24.5	404	1	ICB6_CANEA
9	180.5	24.0	405	1	ICB6_HORSE
10	180.5	24.0	480	1	ICB6_MOUSE
11	179.5	23.9	277	1	ICB3_HUMAN
12	178	23.7	366	1	ICB6_XENTIA
13	176	23.4	402	1	ICB6_RAT
14	175.5	23.3	382	1	ICB6_XENTIA
15	175.5	23.3	410	1	ICB6_FELICA
16	175	23.3	339	1	ICB6_DROME
17	175	23.3	404	1	ICB6_PIG
18	175	23.3	418	1	ICB5_HUMAN
19	173	23.0	402	1	ICB6_MOUSE
20	172.5	22.9	277	1	ICB3_RAT
21	169	22.5	303	1	ICB7_MOUSE
22	169	22.5	419	1	ICB6_MOUSE
23	169	22.5	479	1	ICB8_HUMAN
24	168	22.3	377	1	ICB7_MESAU
25	168	22.3	377	1	ICB4_HUMAN
26	167	22.2	416	1	ICB9_HUMAN
27	166	22.1	303	1	ICB7_HUMAN
28	165.5	22.0	277	1	ICB3_CRILLO
29	165	21.9	373	1	ICB4_MOUSE
30	163	21.7	377	1	ICED_BOVIN
31	162.5	21.6	276	1	ICB3_MOUSE
32	153	20.3	299	1	ICB6_MOUSE
33	153	20.3	299	1	ICB1_SPOK

34	151.5	20.1	521	1	ICB6_HUMAN	Q92851 homo sapien
35	151	20.1	323	1	ICB1_DROME	O02002 drosophila
36	151	20.1	503	1	ICB3_CAEFL	P42573 caenorhabdi
37	145.5	19.3	496	1	ICB3_CAEFL	P45436 caenorhabdi
38	138	18.4	293	1	ICB6_HUMAN	P55212 homo sapien
39	136.5	18.2	282	1	ICB3_XENTIA	P55866 xenopus lae
40	84.5	11.2	520	1	ICB6_MOUSE	O06834 aquilifex
41	82.5	11.0	167	1	ICB3_GALUS	O08814 galdiera s
42	82	10.9	484	1	ICB6_MOUSE	O35732 m casp
43	79.5	10.6	2779	1	LVA_DROME	O08851 drosophila
44	79	10.5	480	1	ICB6_HUMAN	O15519 h casp
45	79	10.5	510	1	ERS3_CERAE	Q9TU32 ceratophthec

ALIGNMENTS

RESULT 1
ICB6_HUMAN
ID ICB6_HUMAN STANDARD; PRT; 242 AA.
AC P31944; 095823;
DT 01-JUL-1993 (Rel. 26, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14).
GN CASP14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22168928; PubMed=12181750;
RA Pistrillo G., Jost M., Srinivasula S.M., Baffa R., Poyet J.-L.,
RA Kari C., Lazebnik Y., Rodeck U., Alnemri E.S.;
RT "Expression and transcriptional regulation of caspase-14 in simple
RT and complex epithelia."
RL Cell Death Differ. 9:995-1006(2002).
RN [2]
RP SEQUENCE OF 68-74; 137-147 AND 154-162.
RC TISSUE=Keratinocytes;
RX MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
RA Vandekerckhove J.; 145 proteins recorded in the two-dimensional gel
RT "Microsequences of normal human epidermal keratinocytes."
RL Electrophoresis 13:960-969(1992).
CC -!- FUNCTION: May be involved in the death receptor and granzyme B
CC apoptotic pathways. May function as a downstream signal transducer
CC of cell death.
CC -!- SUBUNIT: May dimerize with large prodomain caspases.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC
CC -----
CC EMBL; AF097874; AADI6173.1; -
CC PIR; JC7517; JC7517.
CC HSSP; P29466; IICE.
CC Aarhus/Ghent-2DPAGE; 6109; IEF.
CC MEROPS; C14.018; -
CC Genew; HGNC:1502; CASP14.
CC MIM; 605848; -
CC GO; GO:0004199; F:caspase activity; TAS.
CC GO; GO:0008544; P:epidermal differentiation; TAS.
CC InterPro; IPR002138; ICE_p10.

DR InterPro; IPR001309; ICE_p20.
 DR InterPro; IPR002398; Peptidase C14.
 DR Pfam; PF00656; Peptidase C14; 1.
 DR PRINTS; PR00376; IL1BCENZYM.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_HIS; FALSE_NEG.
 DR PROSITE; PS01122; CASPASE_CYS; FALSE_NEG.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR Hydrolyase; Thiol protease; Apoptosis; Zymogen.
 FT CHAIN 1 2
 FT CHAIN 147 242
 FT ACT_SITE 89 BY SIMILARITY.
 FT ACT_SITE 132 132 BY SIMILARITY.
 SQ SEQUENCE 242 AA; 27679 MW; E539FE7EBD808A2 CRC64;
 Query Match 99.3%; Score 747; DB 1; Length 242;
 Best Local Similarity 99.3%; Pred. No. 4.5e-61;
 Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLALHEMRQLEFESTMKRDPTAAQ 60
 Db 1 MSNPRSLSEEEKYDMSGARLILCVTKAREGSEEDLALHEMRQLEFESTMKRDPTAAQ 60
 QY 61 FOELEKFOQALDSREDPVSCAFVLMAGHGEFLKGEDEGMVLEMLFEALNNKNCAL 120
 Db 61 FOELEKFOQALDSREDPVSCAFVLMAGHGEFLKGEDEGMVLEMLFEALNNKNCAL 120
 QY 121 RAKPKVYIIQACRGEORDPGETVGGD 146
 Db 121 RAKPKVYIIQACRGEORDPGETVGGD 146
 RESULT 2
 ICEE MOUSE STANDARD; PRT; 257 AA.
 AC 089094;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-OCT-2001 (Rel. 40, Last sequence update)
 DB Caspase-14 precursor (EC 3.4.22.-) (CASP-14) (MICE).
 GN CASP14.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN 1
 RP SOURCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=99040667; PubMed=9823333;
 RA Ahmed M., Srinivasula S.M., Hegde R., Mukattash R.,
 RA Fernandes-Alnemri T., Alnemri E.S.,
 RT "Identification and characterization of murine caspase-14, a new
 RT member of the caspase family."
 RL Cancer Res. 58:5201-5205(1998).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6; TISSUE=Embryo;
 RC MEDLINE=99222069; PubMed=10203698;
 RA Van de Craen M., Van Loo G., Pype S., Van Criekinge W.,
 RA Van den brande I., Kolemans F., Fiers W., Declercq W.,
 RA Vandenabeele P.,
 RT "Identification of a new caspase homologue: caspase-14."
 RL Cell Death Differ. 5:838-846(1998).
 RL [3]
 RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-136.
 RX MEDLINE=99009076; PubMed=9792675;
 RA Hu S., Snipas S.D., Vincenz C., Salvesen G., Dixit V.M.,
 RT "Caspase-14 is a novel developmentally regulated protease."
 RL J. Biol. Chem. 273:29648-29653(1998).
 CC -1- FUNCTION: Seems to be involved in the death receptor and granzyme
 CC B apoptotic pathways. May function as a downstream signal

CC transducer of cell death. May play a role in ontogenesis and skin
 CC physiology.
 CC -1- SUBUNIT: May dimerize with large prodomain caspases.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
 CC -1- TISSUE SPECIFICITY: Embryo, adult liver and less in adult brain
 CC and kidney.
 CC -1- PM: CLEAVAGE BY GRANZYME B, CASPASE-8 AND -10 GENERATES THE
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 CC PROTEASE.
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -----
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 CC -----
 DR EMBL; AF092997; AAC63364.1; -.
 DR EMBL; AJ007750; CAA07678.1; -.
 DR HSRP; P29466; IICE.
 DR MEROPS; C14.018; -.
 DR MGP; MGI:1335092; Casp14.
 DR GO; GO:0006917; P:induction of apoptosis; IDA.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR Pfam; PF00656; Peptidase C14.
 DR PRINTS; PR00376; IL1BCENZYM.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS01121; CASPASE_HIS; FALSE_NEG.
 DR PROSITE; PS01122; CASPASE_CYS; FALSE_NEG.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR Hydrolyase; Thiol protease; Apoptosis; Zymogen.
 FT PROPEP 1 7
 FT CHAIN 8 257
 FT CHAIN 93 93
 FT ACT_SITE 136 136
 FT ACT_SITE 136 136
 FT MUTAGEN C->A: DECREASE IN DEATH-INDUCING
 FT ACTIVITY.
 SQ SEQUENCE 257 AA; 29458 MW; A228D88DFBA0EB84 CRC64;
 Query Match 77.9%; Score 586; DB 1; Length 257;
 Best Local Similarity 76.0%; Pred. No. 2.3e-46;
 Matches 111; Conservative 18; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLALHEMRQLEFESTMKRDPTAAQ 60
 Db 5 MSNPRSLSEEEKYDMSGARLILCVTKAREGSEEDLALHEMRQLEFESTMKRDPTAAQ 64
 QY 61 FOELEKFOQALDSREDPVSCAFVLMAGHGEFLKGEDEGMVLEMLFEALNNKNCAL 120
 Db 65 FLEELDFEQOTIDNMEFPVSCAFVLMAGHGEFLKGEDEGMVLEMLFEALNNKNCAL 124
 QY 121 RAKPKVYIIQACRGEORDPGETVGGD 146
 Db 125 RAKPKVYIIQACRGEORDPGETVGGD 150
 RESULT 3
 ICEE CHICK STANDARD; PRT; 424 AA.
 AC 098943;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-
 DE IL/IS).
 GN CASP2 OR ICH1.

```

Best local Similarity    35.1%;   Pred. No.6,3e-13;
Matches    52;      Conservative    29;   Mismatches    45;   Indels    22;   Gaps    4;

QY          1 MSNPRSLIEBKRYDMSGALLIILIC-----VTKAREGGSEEDLDALHEMROLRPSESTM 52
           : ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          166 ISEFR-----GLALLISNIHFSSSEKDLEYRSGGVDDASLLELKHYGYVTV 213
           : ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY          53 KRPPTAEFOBELEKFOAIDSRDPVSCAFVMMAIGREGFILKGDEDMWKLNTLFPAL 112
           : ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          214 PHDSAAEEMSALERFESKLPD-HQDVDC-IVALLSHVEGGYGVTCKLLQLGAFLPLF 271
           : ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY          113 NNKNCAALRAKPXYVIIQACRGEGRDPC 140
           : ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          272 DNANCPYLQNKPKMFIFIQACGDDETDRG 299
           : ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4
ICE2_HUMAN STANDARD; PRT; 435 AA.
AC P42575; P42576;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-1L/1S).
GN CASP2 OR ICH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Fetal brain;
RX MEDLINE=94373811; PubMed=8087842;
RA Wang L., Miura M., Bergeron J., Zhu H., Yuan J.;
RT "Ich-1, an Ice/ced-3-related gene, encodes both positive and negative regulators of programmed cell death.";
RL Cell 78:739-750(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS LEU-155; ALA-161 AND GLY-424.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W., Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schwickwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Doeberer A., Martinka S., Maupin R.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP CLEAVAGE SITES
RX MEDLINE=96206041; PubMed=8654923;
RA Xue D., Shamam S., Horvitz H.R.;
RT "The Caenorhabditis elegans cell-death protein CED-3 is a cysteine protease with substrate specificities similar to those of the human CPP32 protease.";
RL Gene Dev. 10:1073-1083(1996).
CC -1- FUNCTION: Involved in the activation cascade of caspases responsible for apoptosis execution. Might function by either activating some proteins required for cell death or inactivating proteins necessary for cell survival.
CC SUBUNIT: Heterodimer of a small and a large subunit (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Isoforms differ in the N- and C-terminal;
CC Name=ICH-1L;
CC IsoId=P42575-1; Sequence=displaced;
CC Note=Acts as a positive regulator of apoptosis;
CC Name=ICH-1S;
CC IsoId=P42575-2; Sequence=VSP_000801, VSP_000802;
CC Note=Acts as a negative regulator of apoptosis;
CC -1- TISSUE SPECIFICITY: Expressed in larger amounts in the embryonic

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CC lung, liver and kidney than in the heart and brain. In the adults
CC higher level expression is seen in the placenta, lung, kidney,
CC pancreas than in the heart, brain, liver and skeletal muscle.
CC -1- PTM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
CC THAT OF OTHER CASPASES.
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -----
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CC -----
DR EMBL; U13021; AAA58959.1; -
DR EMBL; U13022; AAA58960.1; -
DR EMBL; AY219042; AA025653.1; -
DR EMBL; AC073342; AAP22346.1; -
DR PIR; A54821; A54821.
DR HSSP; P29466; 1ICE.
DR MEROPS; C14.006; -
DR Genew; HGNC:1503; CASP2.
DR MIM; 600639; -
DR GO; GO:0004202; F:caspase-2 activity; TAS.
DR GO; GO:0019899; F:enzyme binding; ISS.
DR GO; GO:0008632; P:apoptotic program; TAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCENTME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS02099; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HTS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; Apoptosis; Zymogen; Polymorphism;
KW Alternative splicing.
FT PROPEP 1 152
FT CHAIN 153 308 CASPASE-2 SUBUNIT P18.
FT PROPEP 309 316
FT CHAIN 317 435 CASPASE-2 SUBUNIT P13.
FT CHAIN 331 435 CASPASE-2 SUBUNIT P12.
FT DOMAIN 15 103 CARD.
FT ACT_SITE 260 260 BY SIMILARITY.
FT ACT_SITE 303 303 BY SIMILARITY.
FT VARSPIC 1 14 Missing (in isoform ICH-1S).
FT VARSPIC 306 435 DETRGVDDQDGNHAGSPGCESDAGKEKLPKRLPTSD
VARSPIC 306 435 MLCGYALGKTAMRTKGSWYIEALAVFSPACDMHYA
VARSPIC 306 435 DMIVKVALIKDRBGVAPGTFPHRCKMEKSEVSTICRHLYL
VARSPIC 306 435 PFGHPPT -> GGAIGSLHLLFLTRATSLAL (in
VARSPIC 306 435 isoform ICH-1S).
VARSPIC 306 435 /FTId=VSP_000802.
VARSPIC 306 435 V -> L.
VARSPIC 306 435 /FTId=VAR_016334.
VARSPIC 306 435 P -> A.
VARSPIC 306 435 /FTId=VAR_016335.
VARSPIC 306 435 R -> G.
VARSPIC 306 435 /FTId=VAR_016336.
VARSPIC 306 435 C->S: LOSS OF FUNCTION.
VARSPIC 306 435 A->T: LOSS OF FUNCTION.
VARSPIC 306 435 1652EC73F6286FB7 CRC64;
SQ SEQUENCE 435 AA; 48855 MW; 1652EC73F6286FB7 CRC64;
Query Match 27.9%; Score 210; DB 1; Length 435;
Best Local Similarity 37.5%; Fred. No. 8.1e-12;

Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;
QY 29 REGSEEDLDAEHMFROCFESTWKRDPYAFQFQEBELFOQALDSRDPVSCAFVYMA 88
DB 202 RSGGDVHSTLVTLFLLGLGVHVHLCDTAQMCKLQNFQ-IPIHRYVDS-C-IVALLS 259
QY 89 HGRGFLKGEDEWVKLENLFALNNKQALRAKPKVYIIOACRGQRDPG 140
DB 260 HGVEGAIYGVDKLLOLQEVFQFLDMNCPSTQNKPKKFFIQACRGDETDNG 311
RESULT 5
ICE2 MOUSE
ID ICE2 MOUSE STANDARD; PRT; 435 AA.
AC P29594; 008737;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (NEBD2
DN protein).
GN CASP2 OR ICH1 OR NEBD2 OR NEBD-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=95047319; PubMed=7958843;
RA Kumar S., Kinoshita M., Noda M., Copeland N.G., Jenkins N.A.;
RT "Induction of apoptosis by the mouse Nedd2 gene, which encodes a
RT protein similar to the product of the Caenorhabditis elegans cell
RT death gene ced-3 and the mammalian IL-1 beta-converting enzyme.";
RL Genes Dev. 8:1613-1626(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/Ar.
RX MEDLINE=97190206; PubMed=9039361;
RA van de Craen M., Vandenaabee P., Declercq W., van den Brande I.,
RA van Ioo G., Molemans F., Schotte P., van Criekinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
RN [3]
RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92328780; PubMed=1378265;
RA Kumar S., Tomooka Y., Noda M.;
RT "Identification of a set of genes with developmentally down-regulated
RT expression in the mouse brain.";
RL Biochem. Biophys. Res. Commun. 185:1155-1161(1992).
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Might function by either
CC activating some proteins required for cell death or inactivating
CC proteins necessary for cell survival. May be important in
CC multistep carcinogenesis.
CC -1- SUBUNIT: Heterodimer of a small and a large subunit (By
CC similarity).
CC -1- TISSUE SPECIFICITY: High level expression seen in the embryonic
CC CNS, liver, lung, kidney, small intestine, and hair follicles of
CC skeletal muscle. Moderate expression seen in the skin, oral mucosa,
CC is highly expressed in spleen, lung and thymus. In the adult, it
CC brain, heart, testis, liver. Low levels in the thymus, skeletal
CC muscle, ovary and gut.
CC -1- DEVELOPMENTAL STAGE: During embryonic development is highly
CC expressed in several types of mouse tissue undergoing high rates
CC of programmed cell death such as central nervous system and
CC kidney.
CC -1- PTM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
CC THAT OF OTHER CASPASES (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -1- SIMILARITY: Contains 1 CARD domain.

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CC -----
DR EMBL: D28492; BAA25876.1; ALT INIT.
DR EMBL: Y13085; CAA73527.1; ALT_INIT.
DR HSSP: P42574; IC93.
DR MEROPS: C14.006; -.
DR MGD: MGI:97295; Casp2.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR002138; ICE p10.
DR InterPro: IPR001309; ICE p20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00656; Peptidase_C14; 1.
DR PRINTS: PR00376; ILIBENZYM.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00115; CASc; 1.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
DR KX: Hydroxylase; Thiol protease; Apoptosis; Zymogen.
DR FT: PROPEP 1 152 BY SIMILARITY.
DR FT: CHAIN 153 316 CASPASE-2 SUBUNIT P18 (BY SIMILARITY).
DR FT: CHAIN 317 435 CASPASE-2 SUBUNIT P13 (BY SIMILARITY).
DR FT: CHAIN 331 435 CASPASE-2 SUBUNIT P12 (BY SIMILARITY).
DR FT: DOMAIN 15 103 CARD.
DR FT: ACT_SITE 260 260 BY SIMILARITY.
DR FT: ACT_SITE 303 303 C->G: LOSS OF FUNCTION.
DR FT: MUTAGEN 303 303 MISSING (IN REF. 1).
DR FT: CONFLICT 71 71
DR SQ: SEQUENCE 435 AA; 48896 MW; 8984E6AA767A676 CRC64;

Query Match 27.5%; Score 207; DB 1; Length 435;
Best Local Similarity 37.5%; Pred. No. 1.5e-11;
Matches 42; Conservative 27; Mismatches 41; Indels 2; Gaps 2;

QY 29 REGSEEDLALHEMFROLPESTMKRDPFAEQFOEIELEKFOALDSREDPVSCAFVYVMA 89
DB 202 RSGGDVHTLVTLFKLIGNVHLYDQTAQEMQKLNPAQ-LPAHRTDSCV-VALLS 259
QY 89 HGRBGLKEDGEMVKLENTFEALNNKNCQALPAKPKVYIIQAQGRGORDPG 140
DB 260 HGEVGGIYVDKLLQLOEYVRLFDNANCPSLONKPKMFIIQAQGRGDETRG 311

RESULT 6
ICE2 RAT STANDARD; PRT; 312 AA.
ID ICE2 RAT
AC P55215; O35398;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease)
DE (Fragment).
DE CASP2 OR ICH1.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RS SEQUENCE OF 1-257 FROM N.A.
RC TISSUE=Kidney cortex;
RX MEDLINE=98191309; PubMed=9530276;
RA Kaushal G.P., Singh A.B., Shah S.V.;
RT "Identification of gene family of caspases in rat kidney and altered

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RT expression in ischemia-reperfusion injury.";
RN Am. J. Physiol. 274:F587-F595(1998).
RN [2]
RN RP SEQUENCE OF 131-312 FROM N.A.
RN RC TISSUE=Ovary;
RX MEDLINE=96042508; PubMed=7588240;
RA Flaws J.A., Kugu K., Trbovich A.M., Desanti A., Tilly K.I.,
RA Hirschfeld A.N., Tilly J.L.;
RT "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and
RT mammalian cell death: dissociation of IRP-induced oligonucleosomal
RT endonuclease activity from morphological apoptosis in granulosa cells
RT of the ovarian follicle.";
RL Endocrinology 136:5042-5053(1995).
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Might function by either
CC activating some proteins required for cell death or inactivating
CC proteins necessary for cell survival (By similarity).
CC -1- SUBUNIT: Heterodimer of a small and a large subunit (By
CC similarity).
CC -1- PTM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
CC THAT OF OTHER CASPASES (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -----
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CC -----
DR EMBL: AF025671; AAB82567.1; -.
DR EMBL: U34684; AAC52260.1; -.
DR PIR: I67436; I67436.
DR HSSP: P29466; 1ICE.
DR MEROPS: C14.006; -.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001309; ICE_p20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00656; Peptidase_C14; 1.
DR PRINTS: PR00376; ILIBENZYM.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00115; CASc; 1.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
DR PROSITE: PS01122; CASPASE_HIS; 1.
DR PROSITE: PS01121; CASPASE_P10; 1.
DR Hydroxylase; Thiol protease; Apoptosis; Zymogen.
DR FT: NON_TER 1 1
DR FT: CHAIN 267 312 CASPASE-2 SUBUNIT P18 (BY SIMILARITY).
DR FT: CHAIN 281 312 CASPASE-2 SUBUNIT P13 (BY SIMILARITY).
DR FT: CHAIN 281 312 CASPASE-2 SUBUNIT P12 (BY SIMILARITY).
DR FT: DOMAIN <1 55 CARD.
DR FT: ACT_SITE 210 210 BY SIMILARITY.
DR FT: ACT_SITE 253 253 BY SIMILARITY.
DR FT: NON_TER 312 312
DR SQ: SEQUENCE 312 AA; 35070 MW; 318A0746212E9646 CRC64;

Query Match 27.3%; Score 205; DB 1; Length 312;
Best Local Similarity 37.5%; Pred. No. 1.6e-11;
Matches 42; Conservative 27; Mismatches 41; Indels 2; Gaps 2;

QY 29 REGSEEDLALHEMFROLPESTMKRDPFAEQFOEIELEKFOALDSREDPVSCAFVYVMA 89
DB 152 RSGGDVHTLVTLFKLIGNVHLYDQTAQEMQKLNPAQ-LPAHRTDSCV-VALLS 209
QY 89 HGRBGLKEDGEMVKLENTFEALNNKNCQALPAKPKVYIIQAQGRGORDPG 140
DB 210 HGEVGGIYVDKLLQLOEYVRLFDNANCPSLONKPKMFIIQAQGRGDETRG 261

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RESULT 7
ID 11BC_HUMAN STANDARD; PRT; 404 AA.
AC P29466;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Interleukin-1 beta converting enzyme precursor (IL-1BC) (EC 3.4.22.36) (IL-1
DE beta converting enzyme) (ICE) (Interleukin-1 beta converting enzyme)
DE (P45) (Caspase-1) (CASP-1).
GN CASP1 OR IL1BC OR IL1BCE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND ACTIVE SITE.
RA MEDLINE=92244338; PubMed=1574116;
RA Thornberry N.A., Bull H.G., Calaycay J.R., Chapman K.T., Howard A.D.,
RA Kostura M.J., Miller D.K., Molineaux S.M., Weidner J.R., Aunins U.,
RA Elliston K.O., Ayala J.M., Casano F.J., Chin J., Ding G.J.-F.,
RA Egger L.A., Gaffney E.P., Limjoco G., Palyna O.C., Raju M.,
RA Molando A.M., Salley J.P., Yamin T.-T., Lee T.D., Shively J.E.,
RA McCross M., Mumford R.A., Schmidt J.A., Tocci M.J.,
RT "A novel heterodimeric cysteine protease is required for
RT interleukin-1 beta processing in monocytes."
RL Nature 356:768-774 (1992).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE OF 120-142.
RA MEDLINE=92229430; PubMed=1373520.
RA Corretti D.P., Kozlosky C.J., Mosley B., Nelson N., Van Ness K.,
RA Greenstreet T.A., March C.J., Kronheim S.R., Druck T.,
RA Camarazzo L.A., Huebner K., Black R.A.,
RT "Molecular cloning of the interleukin-1 beta converting enzyme."
RL Science 256:97-100 (1992).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RA MEDLINE=94320145; PubMed=8044845;
RA Walker N.P.C., Talianian R.V., Brady K.D., Dang L.C., Bump N.J.,
RA Ferenz C.R., Franklin S., Ghayur T., Hackett M.C., Hammill L.D.,
RA Herzog L., Huganir M., Houy W., Mankovich J.A., McGinniss L.,
RA Olewicz E., Paskind M., Pratt C.A., Reis P., Sunmani A.,
RA Teranova M., Welch J.P., Xiong L., Moeller A., Tracey D.E., Kamen R.,
RA Wong W.W.,
RT "Crystal structure of the cysteine protease interleukin-1 beta-
RT converting enzyme: a (p20/p10)2 homodimer."
RL Cell 78:343-352 (1994).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.73 ANGSTROMS).
RA MEDLINE=97199458; PubMed=9190283;
RA Rano T.A., Timkey T., Peterson E.P., Rotonda J., Nicholson D.W.,
RA Becker J.W., Chapman K.T., Thornberry N.A.,
RT "A combinatorial approach for determining protease specificities:
RT application to interleukin-1beta converting enzyme (ICE)."
RL Chem. Biol. 4:149-155 (1997).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RA MEDLINE=99142310; PubMed=9987822;
RA Okamoto Y., Anan H., Nakai E., Morihira K., Yonetoku Y., Kurihara H.,
RA Sakashita H., Terai Y., Takeuchi M., Shibamura T., Isonura Y.,
RT "Peptide based interleukin-1 beta converting enzyme (ICE) inhibitors:
RT synthesis, structure activity relationships and crystallographic
RT study of the ICE-inhibitor complex."
RL Chem. Pharm. Bull. 47:11-21 (1999).
RN [6]
RP ALTERNATIVE SPLICING, AND FUNCTION.
RA MEDLINE=95181414; PubMed=7876192;
RA Alnemri E.S., Fernandes-Alnemri T., Litwack G.,
RT "Cloning and expression of four novel isoforms of human interleukin-1
RT beta converting enzyme with different apoptotic activities."
RL J. Biol. Chem. 270:4312-4317 (1995).
CC -!- FUNCTION: Thiol protease that cleaves IL-1 beta between an Asp and
CC an Ala, releasing the mature cytokine which is involved in a

CC variety of inflammatory processes. Specifically inhibited by the
CC compox virus Crma protein.
CC -!- CATALYTIC ACTIVITY: Release of interleukin 1-beta by specific
CC cleavage at 116-Asp|-Ala-117 and 27-Asp|-Gly-28 bonds in
CC precursor. Also hydrolyzes the small-molecule substrate, Ac-Tyr-
CC Val-Ala-Asp|-NHMeC.
CC -!- SUBUNIT: Tetramer that consists of two heterodimers of a 20 kDa
CC (p20) and a 10 kDa (p10) subunits. The p20 subunit can also form a
CC heterodimer with the epsilon isoform which then has an inhibitory
CC effect.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing: Named isoforms=5;
CC Comment=Additional isoforms seem to exist;
CC Name=Alpha;
CC IsoId=P29466-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P29466-2; Sequence=VSP_000798;
CC Name=Gamma;
CC IsoId=P29466-3; Sequence=VSP_000799;
CC Name=Delta;
CC IsoId=P29466-4; Sequence=VSP_000799, VSP_000800;
CC Note=Apoptosis inactive;
CC Name=Epsilon;
CC IsoId=P29466-5; Sequence=VSP_000797;
CC Note=Apoptosis inactive;
CC -!- TISSUE SPECIFICITY: Expressed in larger amounts in spleen and
CC lung. Also found in liver, heart, skeletal muscle, kidney and
CC testis. No expression in the brain.
CC -!- PTM: The two subunits are derived from the precursor sequence by
CC an autocatalytic mechanism.
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL: X65019; CAA46153.1; -
CC EMBL: M87507; AAA66942.1; -
CC EMBL: U13697; AAC50107.1; -
CC EMBL: U13698; AAC50108.1; -
CC EMBL: U13699; AAC50109.1; -
CC EMBL: U13700; AAC50110.1; -
CC PIR: A54263; A42677.
CC PIR: A56084; A56084.
CC PIR: B56084; B56084.
CC PIR: C56084; C56084.
CC PIR: D56084; D56084.
CC PDB: 1ICE; 28-JUL-95.
CC PDB: 1IBC; 11-FEB-98.
CC PDB: 1BQC; 29-JUL-98.
CC MEROPS: C14.001; -.
CC GeneW: HGNC:1495; CASP1.
CC MIM: 147678; -
CC GO: GO:0008656; F:caspace activator activity; TAS.
CC GO: GO:0004201; F:caspace-1 activity; TAS.
CC GO: GO:0006915; P:apoptosis; TAS.
CC GO: GO:0009405; P:apoptogenesis; TAS.
CC GO: GO:0006508; P:proteolysis and peptidolysis; TAS.
CC GO: GO:0007165; P:signal transduction; TAS.
CC InterPro: IPR001315; CARD.
CC InterPro: IPR002138; ICE p10.
CC InterPro: IPR001309; ICE p20.
CC InterPro: IPR002398; Peptidase_C14.
CC Pfam: PF00619; CARD. 1.
CC Pfam: PF00656; Peptidase_C14; 1.
CC PRINTS: PR00376; IL1BCENZYM.
CC SMART: SMO0114; CARD. 1.

DR SMART; SM00115; CASc; 1.
 DR PROSITE; PS50209; CARD; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR Hydrolyase; Thiol protease; Zymogen; 3D-structure;
 KM Alternative splicing.
 FT PROPEP 1 119
 FT CHAIN 120 297 INTERLEUKIN-1 BETA CONVERTASE P20.
 FT PROPEP 298 316
 FT CHAIN 317 404 INTERLEUKIN-1 BETA CONVERTASE P10.
 FT DOMAIN 1 91
 FT ACT_SITE 237 237
 FT ACT_SITE 285 285
 FT VARSPPLIC 20 335
 FT VARSPPLIC 92 112
 FT VARSPPLIC 20 112
 FT VARSPPLIC 20 112
 FT VARSPPLIC 288 335
 FT HELIX 138 148
 FT HELIX 149 151
 FT STRAND 152 152
 FT TURN 158 160
 FT STRAND 164 169
 FT TURN 180 181
 FT TURN 182 196
 FT TURN 197 197
 FT STRAND 199 204
 FT HELIX 208 220
 FT HELIX 222 226
 FT STRAND 230 235
 FT STRAND 238 238
 FT STRAND 242 244
 FT STRAND 246 247
 FT TURN 255 257
 FT STRAND 258 265
 FT HELIX 267 269
 FT TURN 271 273
 FT HELIX 274 275
 FT STRAND 278 283
 FT STRAND 289 289
 FT STRAND 327 331
 FT TURN 335 336
 FT STRAND 337 337
 FT STRAND 340 342
 FT HELIX 343 345
 FT STRAND 346 347
 FT STRAND 348 360
 FT HELIX 361 363
 FT TURN 366 375
 FT HELIX 376 377

Query Match 24.9%; Score 187.5; DB 1; Length 404;
 Best Local Similarity 35.2%; Pred. No. 8.3e-10;
 Matches 51; Conservative 23; Mismatches 52; Indels 19; Gaps 6;

QY 15 SGAAALILICVTK-----AREGSEEDDALEHMRQURFSTMKRDPFAQFOEELKFEQ 69
 DB 160 SRRRLAIIINEEDSDIPRRIGAVDITGMMLQNGYSDVKKNLTASDMTELEFAFA 219
 QY 70 QALDSREDPVSCAFVITMANG-RGFLKGEDEVY---KLENIPELNNKCAALAKP 124
 DB 220 HRPKHKTS--DSTFLVFMHSGIRGICGKKHSEQVPIQLQNALFNNLNTNKCPSLKDGP 277
 QY 125 KVVYIIACRGGRQDPG-----ETWG 144
 DB 278 KVVIIQAKRGD--SPGVVWFKDSVVG 300

RESULT 8
 ID IIBC_CANFA STANDARD; PRT; 404 AA.
 AC Q9MZV7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Interleukin-1 beta converting precursor (IL-1BC) (EC 3.4.22.36) (IL-1
 DE beta converting enzyme) (ICE) (Interleukin-1 beta converting enzyme)
 DE (P45) (Caspase-1) (CASP-1).
 GN CASP1 OR IL1BC.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_Taxid=9615;
 RP MEDLINE=20284946; PubMed=10826695;
 RA Taylor S., Hanlon L., McGillivray C., Gault E.A., Argyle D.J.,
 RA Onions D.E., Nicolson L.;
 RT "Cloning and sequencing of feline and canine ice-related cDNAs
 RT encoding hybrid caspase-1/caspase-13-like propeptides.";
 RL DNA Seq. 10:387-394(2000).
 CC -1- FUNCTION: Thiol protease that cleaves IL-1 beta between an Asp and
 CC an Ala, releasing the mature cytokine which is involved in a
 CC variety of inflammatory processes (By similarity).
 CC -1- CATALYTIC ACTIVITY: Release of interleukin 1-beta by specific
 CC cleavage at 116-Asp-[Ala-117 and 27-Asp-[Gly-28 bonds in
 CC precursor. Also hydrolyzes the small-molecule substrate, Ac-Tyr-
 CC Val-Ala-Asp-[NHMeC.
 CC -1- SUBUNIT: Tetramer that consists of two heterodimers of a 20 kDa
 CC (p20) and a 10 kDa (p10) subunits. The p20 subunit can also form a
 CC heterodimer with the epsilon isoform which then has an inhibitory
 CC effect (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to the precursor sequence by
 CC an autocatalytic mechanism
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -1- SIMILARITY: Contains 1 CARD domain.
 CC
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF135967; AAF64388.1; -.
 DR HSSP; P29466; IICE.
 DR MEROPS; C14.024; -.
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; IL1BCENZME.
 DR SMART; SM00114; CARD; 1.
 DR SMART; SM00115; CASc; 1.
 DR PROSITE; PS50209; CARD; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 KM Hydrolyase; Thiol protease; Zymogen.
 FT PROPEP 1 119
 FT CHAIN 120 297 INTERLEUKIN-1 BETA CONVERTASE P20.
 FT PROPEP 298 316
 FT CHAIN 317 404 INTERLEUKIN-1 BETA CONVERTASE P10.
 FT DOMAIN 1 91
 FT ACT_SITE 237 237
 FT ACT_SITE 237 237

FT ACT SITE 285 285 BY SIMILARITY.
SQ SEQUENCE 404 AA; 45662 MW; BCSA505CD7DBDFDD CRC64;
Query Match 24.5%; Score 184; DB 1; Length 404;
Best Local Similarity 33.8%; Pred. No. 1.7e-09;
Matches 46; Conservative 27; Mismatches 43; Indels 20; Gaps 5;
QY 19 LALLICVTK----AREGSEBDLALHEMFRLPFEFTMKRDPFAEQEELKFOQAID 73
DB 164 LALLICIEFDHLSTRDGAEDIDAGMESILEGLGYSVVKKLLAKMGESVLRFAFARPE 223
QY 74 SREDPVCAPFVYLMAGREGFLK-----EDGEVKLENLPEALNNKXQALRAKPK 125
DB 224 HKSS--DSTFLVMSH---GLINGICGTANSVENPDVLAVDITIPINRRLMLKDKPK 278
QY 126 VYIIQACRGEDRDE 141
DB 279 VTIIOACRGE--NGE 292
RESULT 9
IIBC HORSE
ID IIBC HORSE STANDARD; PRT; 405 AA.
AC 09TVL3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Interleukin-1 beta convertase precursor (IL-1BC) (EC 3.4.22.36) (IL-1 beta converting enzyme) (ICE) (Interleukin-1 beta converting enzyme) (P45) (Caspase-1) (CASP-1).
GN CASP1 OR IIBC.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxId=9796;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99304505; PubMed=10376217;
RA Wardlaw S., Penha-Goncalves M.N., Aryle D.J., Onions D.E., Nicolson L.;
RT "Nucleotide sequence of equine caspase-1 cDNA."
RL DNA Seq. 10:133-137(1999).
CC -1- FUNCTION: Thiol protease that cleaves IL-1 beta between an Asp and an Ala, releasing the mature cytokine which is involved in a variety of inflammatory processes (By similarity).
CC -1- CATALYTIC ACTIVITY: Release of interleukin-1-beta by specific cleavage at 116-Asp-Ala-117 and 27-Asp-Gly-28 bonds in Val-Ala-Asp-NHMeC
CC -1- SUBUNIT: Tetramer that consists of two heterodimers of a 20 kDa (p20) and a 10 kDa (p10) subunits. The p20 subunit can also form a heterodimer with the epsilon isoform which then has an inhibitory effect (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: The two subunits are derived from the precursor sequence by an autocatalytic mechanism.
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -1- SIMILARITY: Contains 1 CARD domain.
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CC -----
DR EMBL; AF090119; AAD46400.1; --
DR HSRP; P29466; IICE.
DR MEROPS; C14.001; --
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.

DR InterPro; IPR002198; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IILBCENZYE.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; Case; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS_1.
DR PROSITE; PS01121; CASPASE_HIS_1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; zymogen; Polymorphism.
FT PROPEP 1 119 POTENTIAL.
FT CHAIN 120 298 INTERLEUKIN-1 BETA CONVERTASE P20.
FT PROPEP 299 317 POTENTIAL.
FT CHAIN 318 405 INTERLEUKIN-1 BETA CONVERTASE P10.
FT DOMAIN 1 91 CARD.
FT ACT SITE 238 238 BY SIMILARITY.
FT ACT SITE 286 286 BY SIMILARITY.
FT VARIANT 203 203 V -> L.
FT VARIANT 305 305 N -> S.
SQ SEQUENCE 405 AA; 45331 MW; 7CE8729B359CC17 CRC64;
Query Match 24.0%; Score 180.5; DB 1; Length 405;
Best Local Similarity 34.3%; Pred. No. 3.6e-09;
Matches 49; Conservative 24; Mismatches 53; Indels 17; Gaps 5;
QY 10 ERYDMGAA----LALLICVTK----AREGSEBDLALHEMFRLPFEFTMKRDPFAE 59
DB 151 EWPYIMGKSWTRRLIILICNTFEDNLSRAGAEDVIAKVKVLEGGYGVEXENTLAL 210
QY 60 QFOEELKFOQALDSREDPVCAPFVYLMAG-REGFLKSGDEMY---KLENLFEALNN 114
DB 211 DMTTEKAPAPAREHSS--DSTFLVMSHIGREICGKKSEKVPDVLVNTTFOIENT 268
QY 115 KNCQALRAKPYIIIOACRGQR 137
DB 269 RNCPNLRDKPKVILIIQACRGENG 291
RESULT 10
ICE8 MOUSE
ID ICE8 MOUSE STANDARD; PRT; 480 AA.
AC 0891I0; O35669;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
GN Caspase-8 precursor (EC 3.4.22.-).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
[1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX STRAIN=129/SVJ;
RC MEDLINE=98316661; PubMed=9654089;
RA Sakamaki K., Tsukumo S.-I., Yonehara S.;
RT "Molecular cloning and characterization of mouse caspase-8."
RL Eur. J. Biochem. 253:399-405(1998).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=99057979; PubMed=9837723;
RA Van de Craen M., Van Loo G., Declercq W., Schotte P., Vandenabeele P.;
RA "Molecular cloning and identification of murine caspase-8."
RT J. Mol. Biol. 284:1017-1026(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N, TISSUE=Colon, and Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner I., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buehler K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Cavaant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Cantucci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abrahamson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shechenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [4]
 RN SEQUENCE OF 57-476 FROM N.A.
 RP Kioschis P., Kischkel P., Poustka A., Krammer P.,
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Most upstream protease of the activation cascade of
 CC caspases responsible for the TNFRSF6/FAS mediated and TNFRSF1A
 CC induced cell death. Binding to the adapter molecule FADD recruits
 CC it to either receptor. The resulting aggregate called death-
 CC inducing signaling complex (DISC) performs CASP8 proteolytic
 CC activation. The active dimeric enzyme is then liberated from the
 CC DISC and free to activate downstream apoptotic proteases.
 CC Proteolytic fragments of the N-terminal propeptide (termed CAP3,
 CC CAP5 and CAP6) are likely retained in the DISC. Cleaves and
 CC activates CASP3, CASP4, CASP6, CASP7, CASP9 and CASP10. May
 CC participate in the G2M4 apoptotic pathways. Cleaves APOPT.
 CC Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-|-AMC.
 CC Likely target for the complex virus CRMA death inhibitory protein.
 CC -1- ENZYME REGULATION: Inhibited by Z-VAD-FK, Crma and P35.
 CC -1- SUBUNIT: Heterodimer of a 18 kDa (P18) and a 10 kDa (P10) subunit.
 CC -1- INTERACTIONS: Interacts with FADD, Cflar and Peals (By similarity).
 CC -1- TISSUE SPECIFICITY: Expressed in a wide variety of tissues.
 CC Highest expression in spleen, thymus, lung, liver and kidney.
 CC Lower expression in heart, brain, testis and skeletal muscle.
 CC -1- DEVELOPMENTAL STAGE: In the embryo, highest expression occurs at
 CC day 7.
 CC -1- PTM: Generation of the subunits requires association with the
 CC death-inducing signaling complex (DISC), whereas additional
 CC processing is likely due to the autocatalytic activity of the
 CC activated protease. GZMB and CASP10 can be involved in these
 CC processing events. (By similarity).
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -1- SIMILARITY: Contains 2 death effector (DED) domains.
 CC -----
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 CC -----
 DR EMBL: AF067841; AAC40132.1; -
 DR EMBL: AF067845; AAC40132.1; JOINED.
 DR EMBL: AF067846; AAC40132.1; JOINED.
 DR EMBL: AF067847; AAC40132.1; JOINED.
 DR EMBL: AF067848; AAC40132.1; JOINED.
 DR EMBL: AF067849; AAC40132.1; JOINED.
 DR EMBL: AF067850; AAC40132.1; JOINED.
 DR EMBL: AF067851; AAC40132.1; JOINED.
 DR EMBL: AF067852; AAC40132.1; JOINED.
 DR EMBL: AF067853; AAC40132.1; JOINED.
 DR EMBL: AF067854; AAC40132.1; JOINED.
 DR EMBL: AF067855; AAC40132.1; JOINED.
 DR EMBL: AF067856; AAC40132.1; JOINED.
 DR EMBL: AF067857; AAC40132.1; JOINED.
 DR EMBL: AF067858; AAC40132.1; JOINED.
 DR EMBL: AF067859; AAC40132.1; JOINED.
 DR EMBL: AF067860; AAC40132.1; JOINED.
 DR EMBL: AF067861; AAC40132.1; JOINED.
 DR EMBL: AF067862; AAC40132.1; JOINED.
 DR EMBL: AF067863; AAC40132.1; JOINED.
 DR EMBL: AF067864; AAC40132.1; JOINED.
 DR EMBL: AF067865; AAC40132.1; JOINED.
 DR EMBL: AF067866; AAC40132.1; JOINED.
 DR EMBL: AF067867; AAC40132.1; JOINED.
 DR EMBL: AF067868; AAC40132.1; JOINED.
 DR EMBL: AF067869; AAC40132.1; JOINED.
 DR EMBL: AF067870; AAC40132.1; JOINED.
 DR EMBL: AF067871; AAC40132.1; JOINED.
 DR EMBL: AF067872; AAC40132.1; JOINED.
 DR EMBL: AF067873; AAC40132.1; JOINED.
 DR EMBL: AF067874; AAC40132.1; JOINED.
 DR EMBL: AF067875; AAC40132.1; JOINED.
 DR EMBL: AF067876; AAC40132.1; JOINED.
 DR EMBL: AF067877; AAC40132.1; JOINED.
 DR EMBL: AF067878; AAC40132.1; JOINED.
 DR EMBL: AF067879; AAC40132.1; JOINED.
 DR EMBL: AF067880; AAC40132.1; JOINED.
 DR EMBL: AF067881; AAC40132.1; JOINED.
 DR EMBL: AF067882; AAC40132.1; JOINED.
 DR EMBL: AF067883; AAC40132.1; JOINED.
 DR EMBL: AF067884; AAC40132.1; JOINED.
 DR EMBL: AF067885; AAC40132.1; JOINED.
 DR EMBL: AF067886; AAC40132.1; JOINED.
 DR EMBL: AF067887; AAC40132.1; JOINED.
 DR EMBL: AF067888; AAC40132.1; JOINED.
 DR EMBL: AF067889; AAC40132.1; JOINED.
 DR EMBL: AF067890; AAC40132.1; JOINED.
 DR EMBL: AF067891; AAC40132.1; JOINED.
 DR EMBL: AF067892; AAC40132.1; JOINED.
 DR EMBL: AF067893; AAC40132.1; JOINED.
 DR EMBL: AF067894; AAC40132.1; JOINED.
 DR EMBL: AF067895; AAC40132.1; JOINED.
 DR EMBL: AF067896; AAC40132.1; JOINED.
 DR EMBL: AF067897; AAC40132.1; JOINED.
 DR EMBL: AF067898; AAC40132.1; JOINED.
 DR EMBL: AF067899; AAC40132.1; JOINED.
 DR EMBL: AF067900; AAC40132.1; JOINED.
 DR EMBL: AF067901; AAC40132.1; JOINED.
 DR EMBL: AF067902; AAC40132.1; JOINED.
 DR EMBL: AF067903; AAC40132.1; JOINED.
 DR EMBL: AF067904; AAC40132.1; JOINED.
 DR EMBL: AF067905; AAC40132.1; JOINED.
 DR EMBL: AF067906; AAC40132.1; JOINED.
 DR EMBL: AF067907; AAC40132.1; JOINED.
 DR EMBL: AF067908; AAC40132.1; JOINED.
 DR EMBL: AF067909; AAC40132.1; JOINED.
 DR EMBL: AF067910; AAC40132.1; JOINED.
 DR EMBL: AF067911; AAC40132.1; JOINED.
 DR EMBL: AF067912; AAC40132.1; JOINED.
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RP CLEAVAGE OF HUNTINGTIN.
RX MEDLINE=96331285; PubMed=8696339;
RA Goldberg Y.P., Nicholson D.W., Rasper D.M., Kalchman M.A., Koide H.B.,
RA Graham R.K., Bromm M., Kazemi-Esfarjani P., Thornberry N.A.,
RA Vailancourt J.P., Hayden M.R.,
RT "Cleavage of huntingtin by apopain, a proapoptotic cysteine protease,
RT is modulated by the polyglutamine tract.";
RL Nat. Genet. 13:442-449(1996).
RN [12]
RP FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. At the onset of apoptosis it
CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
CC 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory
CC element binding proteins (SREBPs) between the basic helix-loop-
CC helix leucine zipper domain and the membrane attachment domain.
CC Cleaves and activates caspase-6, -7 and -9. Involved in the
CC cleavage of huntingtin.
CC - ENZYME REGULATION: Inhibited by isatin sulfonamides.
CC - SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit.
CC - SUBCELLULAR LOCATION: Cytoplasmic.
CC - TISSUE SPECIFICITY: Highly expressed in lung, spleen, heart, liver
CC and kidney. Moderate levels in brain and skeletal muscle, and low
CC in testis. Also found in many cell lines, highest expression in
CC cells of the immune system.
CC - PTM: CLEAVAGE BY GRANTZYME B, ADAP-1, CASPASE-6, -8 AND -10
CC GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
CC PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
CC ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
CC OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
CC AND VICE VERSA.
CC - SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, U13737; AAA65015.1; -;
DR EMBL, U13738; AAB60355.1; -;
DR EMBL, U26943; AAA74929.1; -;
DR EMBL, AJ413269; CAC88866.1; -;
DR EMBL, AY219866; AAO25654.1; -;
DR EMBL, BC016926; AAH16926.1; -;
DR PIR, A55315; A55315;
DR PDB, 1PAU; 07-JUN-97.
DR PDB, 1CP3; 24-DEC-97.
DR PDB, 1CFW; 23-JUN-00.
DR MEROPS, C14.003; -;
DR Genem; HGNC:1504; CASP3.
DR MIM; 600636; -;

```

DR GO; GO:0004208; F.caspase-3 activity; TAS.
DR GO; GO:0008624; P.induction of apoptosis by extracellular sig. . .; TAS.
DR GO; GO:0008629; P.induction of apoptosis by intracellular sig. . .; TAS.
DR GO; GO:0009405; P.pathogenesis; TAS.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR Hydrolyase; Thiol protease; Zymogen; Apoptosis; Polymorphism;
KM 3D-structure.
FT PROPEP 1 9
FT PROPEP 10 28
FT CHAIN 29 175
FT CHAIN 176 277
FT ACT SITE 121 121
FT ACT SITE 163 163
FT VARIANT 190 190
FT CONFLICT 31 36
FT STRAND 36 36
FT STRAND 43 51
FT HELIX 57 59
FT TURN 60 60
FT TURN 65 66
FT HELIX 67 80
FT TURN 81 82

Query Match 23.9%; Score 179.5; DB 1; Length 277;
Best Local Similarity 30.7%; Pred. No. 2.9e-09;
Matches 46; Conservative 25; Mismatches 60; Indels 19; Gaps 5;

QY 9 EEKYDWSGAALALILCVTK-----AREGSEEDDLALHEMFROJRESTMKRDPYA 58
DB 34 DNGYKMDYPMGCIITNNKNFHKSTGTSRSGTDVDAANLRFTFNKKEVHNKNDLTR 93
QY 59 EOGOELELEKFOQALDSREDVSCAFVYLMAHGREGLKSGDG--EWKLENLFEALNNKN 116
DB 94 EEVEIMRDVSKEDHSKRSSFVC---VLISHGEGGIIFGNPGVDLKKITNFF---RGDR 147
QY 117 COALRAKPYVYIIQACRGQORDPG-ETVGG 145
DB 148 CRSLTGKPKLFIIOACRGTELDGSIETDSG 177

RESULT 12
ICBA_XENLA STANDARD; PRT; 386 AA.
AC P55865;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-1 beta convertase homology A precursor (EC 3.4.22.-)
DE (XICE-A) (Caspase-1A) (CASP-1A).
GN CASP1A.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodidae; Xenopus.
CX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Yacita Y., Nakajima K.;
RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -1- SIMILARITY: Contains 1 CARD domain.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D89783; BA014017.1; -.
DR HSP; P29466; 1ICB.
DR MEROPS; C14.UFW; -.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR Hydrolyase; Thiol protease; Zymogen.
KM 3D-structure.
FT PROPEP 1 9
FT PROPEP 10 28
FT CHAIN 29 175
FT CHAIN 176 277
FT ACT SITE 121 121
FT ACT SITE 163 163
FT VARIANT 190 190
FT CONFLICT 31 36
FT STRAND 36 36
FT STRAND 43 51
FT HELIX 57 59
FT TURN 60 60
FT TURN 65 66
FT HELIX 67 80
FT TURN 81 82

Query Match 23.7%; Score 178; DB 1; Length 386;
Best Local Similarity 29.5%; Pred. No. 5.8e-09;
Matches 49; Conservative 26; Mismatches 57; Indels 34; Gaps 5;

QY 4 PRLEERK-----YDM-----SGAALALILCVTK-----AREGSEEDDLALHEMF 44
DB 116 PCSAEFPKKIOTDQGIYDKRKGKGLALITCNKFNENRGAQKADLDGMKTLN 175
QY 45 QLRFESTMKRDPAEFOELELEKFOQALDSREDVSCAFVYLMAHGREGLKSGDG-- 101
DB 176 ELGQVQHNNLNTKTEMVKVKEF--AAQEHADSDSTFIYLSHSGRGQVCGPDSKTE 233
QY 102 -----WVKLENLFEALNNKNCOALRAKPYVYIIQACRGQR 137
DB 234 KEGQYEVNMLEIDRIFSTFNVNCCKLNKPKVYIIQACRGK 279

RESULT 13
IIBC_RAT STANDARD; PRT; 402 AA.
AC P43527;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-1 beta convertase precursor (IL-1C) (EC 3.4.22.36) (IL-1
DE beta converting enzyme) (ICE) (Interleukin-1 beta converting enzyme)
DE (P45) (Caspase-1) (CASP-1).
GN CASP1 OR IIBC OR IL1BC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Skin;
RC MEDLINE=95299018; PubMed=7780029;
RA Keane K.W., Giegel D.A., Lipinski W.J., Callahan M.J.,
RA Shivers B.D.;
RT "Cloning, tissue expression and regulation of rat interleukin 1 beta
RT converting enzyme.";

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QY      19 LALLILCVT-----KAREGEEDIDALEHMFPRQURFSTAKRDPYTAQFOEELKFOQAIQ 73
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      163 LALLICNTDFQHLISRRVADVDLREKLLTLDQGYTVKKEKNTALEMTKELEFPACPE 222
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      74 SREDPVSCAFVYIMAHG-EEGF-----LKGEDEGMVLELNFELANKNCOALRAKPKVYI 128
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      223 HKTS--DSTFELFVMSHGLQEGICITYSNEVADILKVDITFGQMNTLLKPSLMDKPKVIT 280
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      129 IOACRGEOR 137
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      281 IQACRGEKQ 289
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
ID      ICEB_XENLA          STANDARD:          PRT:      382 AA.
AC      P55867;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Interleukin-1 beta convertase homolog B precursor (EC 3.4.22.-)
DE      (XICE-B) (Caspase-1B) (CASP-1B).
GN      CASP1B.
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=83355;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Nakajima K.;
RL      Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC      -|- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
CC      -|- SIMILARITY: Belongs to peptidase family C14.
CC      -|- SIMILARITY: Contains 1 CARD domain.
-----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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-----
DR      EMBL; D89785; BAAL14019.1; -.
DR      HSSP; P29466; IICE.
DR      MEROPS; C14.1PW/-;
DR      InterPro; IPR001315; CARD.
DR      InterPro; IPR002138; ICE_P10.
DR      InterPro; IPR001309; ICE_P20.
DR      InterPro; IPR002398; Peptidase_C14.
DR      Pfam; PF00619; CARD. 1.
DR      Pfam; PF00656; Peptidase_C14. 1.
DR      PRINTS; PR00376; IILBCENZME.
DR      SMART; SM00114; CARD; 1.
DR      SMART; SM00115; CASC; 1.
DR      PROSITE; PSS0209; CARD; 1.
DR      PROSITE; PSS0122; CASPASE_CYS; 1.
DR      PROSITE; PSS0121; CASPASE_HIS; 1.
DR      PROSITE; PSS0207; CASPASE_P10; 1.
DR      PROSITE; PSS0208; CASPASE_P20; 1.
KW      Hydrolyase; Thiol protease; Zymogen.
FT      PROPEP      1
FT      CHAIN      ?
FT      DOMAIN      22
FT      ACT_SITE    216
FT      ACT_SITE    270
FT      ACT_SITE    270
SQ      SEQUENCE      382 AA; 43389 MW; 81D2FB7BF3C2230F CRC64;

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QY 4 PRSLIEEK-YDMG-----AALALILC-----VTKAREGSEEDLDALEHMR 44
DB 114 PCSAEFEFNKIDYSDHDKIYEVNERGRKRRLALILNETFQSMSERRGAKDLLEGNNKILN 173
QY 45 QLRPESTAKRPDPTAOFQOELEKEFQQAIDSDREDFV--SCAFVYLAHAREGFLKEDGE- 101
DB 174 ELGYVQOQHTNLTKAEWKAKKEFA---AREEHADSDSTFVLSHGDKREVCTIDSK 229
QY 102 -----WKLENTFEALNNKCOALRAKPKYVYIIQACRGQRDPGETVGGD 146
DB 230 TENGYGYTNLLQVEIFSTFNNVNCNSRLMDKPKYIIIIQACGEGNQG--GELYRDD 283

RESULT 15
11BC_FELCA STANDARD; PRT; 410 AA.
ID 11BC_FELCA STANDARD; PRT; 410 AA.
AC 09KZV6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-1 beta convertase precursor (IL-1BC) (BC 3.4.22.36) (IL-1
DE beta converting enzyme) (ICE) (Interleukin-1 beta converting enzyme)
DE (P45) (Caspase-1) (CASP-1).
GN CASP1 OR IL1BC.
OS Felis silvestris catus (cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_Taxid=9695;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20284946; PubMed=10826695;
RA Taylor S., Hanlon L., McGillivray C., Gault E.A., Argyle D.J.,
RA Onions D.B., Nicolson L.;
RT Cloning and sequencing of feline and canine ice-related cDNAs
RT encoding hybrid caspase-1/caspase-13-like propeptides.";
RL DNA Seq. 10:387-394 (2000).
CC -1- FUNCTION: Thiol protease that cleaves IL-1 beta between an Asp and
CC an Ala, releasing the mature cytokine which is involved in a
CC variety of inflammatory processes (By similarity).
CC -1- CATALYTIC ACTIVITY: Release of interleukin 1-beta by specific
CC cleavage at 116-Asp-Ala-117 and 27-Asp-Gly-28 bonds in
CC precursor. Also hydrolyzes the small-molecule substrate, Ac-Tyr-
CC Val-Ala-Asp-NHMe.
CC -1- SUBUNIT: Tetramer that consists of two heterodimers of a 20 kDa
CC (p20) and a 10 kDa (p10) subunits. The p20 subunit can also form a
CC heterodimer with the epsilon isoform which then has an inhibitory
CC effect (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: The two subunits are derived from the precursor sequence by
CC an autocatalytic mechanism.
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -----
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CC -----
DR EMBL; AF135968; AAF64389.1; -.
DR HSSP; P29466; 1ICE.
DR MEROPS; C14.024; -.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; TLBCENZME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASG; 1.

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DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; Zymogen; Polymorphism.
FT CHAIN 1 119
FT PROPEP 120 296
FT CHAIN 120 296
FT PROPEP 297 322
FT CHAIN 323 410
FT DOMAIN 1 91
FT ACT_SITE 235 235
FT ACT_SITE 284 284
FT VARIANT 136 136 H -> R.
SQ SEQUENCE 410 AA; 46051 MW; 2B8B99C0074A0C5 CRC64;

Query Match 23.3%; Score 175.5; DB 1; Length 410;
Best Local Similarity 31.3%; Pred. No. 1,1e-08;
Matches 41; Conservative 26; Mismatches 45; Indels 19; Gaps 4;

QY 19 LALILCVT-----KAREGSEEDLDALEHMRQLREESTMKRPDPTAOFQOELEKEFQQAID 73
DB 162 LALILCVTTFDHLSPKRGADLDVAQMRRLITDGLGVHKEELTKADWSELRAFAAPE 221
QY 74 SREDPVSCAFVYLAHAREGFLKG-----EDGEVWKLNTFEALNNKCOALRAPE 124
DB 222 HKSS--DSFLVFMNH---GILSGICGTKYSAGDPDVLAYDTIFQIFNNRCLSLDKR 276
QY 125 KYVYIIQACRGE 135
DB 277 KYVYIIQACRGE 287

```

Search completed: July 12, 2004, 13:48:22
 Job time : 7.2367 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:43:31 ; Search time 29.8636 Seconds
(without alignments)
1542.533 Million cell updates/sec

Title: US-10-068-564-5_COPY_1_146
Perfect score: 752
Sequence: 1 MSNPRSLREKXDMGSAALA.....YIIQACRGEQRDPETGVGD 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	210	27.9	435	4	Q9BUP7
2	210	27.9	452	11	Q8C9H7
3	207	27.5	452	11	Q8K241
4	205	27.3	452	11	Q55194
5	204.5	27.2	399	13	Q9IB63
6	198	26.3	423	13	Q9IB67
7	197	26.2	312	4	Q86UJ3
8	196	26.1	415	13	Q80UM6
9	196	26.1	419	13	Q7ZXD2
10	195	25.9	403	13	Q90WU0
11	194	25.8	393	11	Q9R0S9
12	194	25.8	453	11	Q8C300
13	194	25.8	454	11	Q9R0T0
14	194	25.8	454	11	Q8C309
15	192	25.5	343	11	Q9WU16
16	191.5	25.5	482	13	Q90WU1

17	191	25.4	402	11	Q8K419	Q8K419 meriones un
18	181.5	24.1	383	13	Q919L7	Q919L7 brachydanio
19	178	23.7	454	11	Q9JHKL	Q9JHKL rattus norv
20	177	23.5	402	11	Q9IW32	Q9IW32 rattus norv
21	175.5	23.3	182	6	Q77623	Q77623 ovis arie
22	174.5	23.2	500	13	Q9IB64	Q9IB64 xenopus lae
23	173.5	23.1	290	13	Q8J1S8	Q8J1S8 oryzias lat
24	173	23.0	303	11	Q88550	Q88550 rattus norv
25	171.5	22.8	277	6	Q8MTU1	Q8MTU1 felis silve
26	171	22.7	316	5	Q817B0	Q817B0 geodia cydo
27	171	22.7	426	5	Q816Y2	Q816Y2 geodia cydo
28	170	22.6	420	11	Q920D5	Q920D5 rattus norv
29	169	22.5	419	11	Q8BSX6	Q8BSX6 mus musculu
30	167	22.2	482	11	Q9JHX4	Q9JHX4 rattus norv
31	167	22.2	520	13	Q9IB62	Q9IB62 xenopus lae
32	165	21.9	373	11	Q91XW7	Q91XW7 rattus norv
33	164.5	21.9	417	5	Q9YIU6	Q9YIU6 pristionchu
34	164.5	21.9	417	5	Q9YIU6	Q9YIU6 sus scrofa
35	163.5	21.7	277	6	Q95NDS	Q95NDS sus scrofa
36	163.5	21.7	277	6	Q8MTC3	Q8MTC3 oryctolagus
37	162.5	21.6	277	6	Q8WK15	Q8WK15 canis fami
38	162.5	21.6	313	11	Q8CHV5	Q8CHV5 mus musculu
39	161.5	21.5	289	5	Q86FLO	Q86FLO anopheles s
40	157	20.9	299	5	Q81955	Q81955 spodoptera
41	156	20.7	318	13	Q9IB65	Q9IB65 xenopus lae
42	156	20.7	383	11	Q99M88	Q99M88 rattus norv
43	155	20.6	283	13	Q93417	Q93417 gallus gall
44	154.5	20.5	476	13	Q918U5	Q918U5 brachydanio
45	154	20.5	293	5	Q819V7	Q819V7 bombyx mori

ALIGNMENTS

RESULT 1
Q9BUP7 PRELIMINARY: PRT; 435 AA.
ID Q9BUP7
AC Q9BUP7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Similar to caspase 2 (Neutral cell expressed, developmentally down-regulated 2).
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin.
RA Strausberg R.;
RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kalnne N., Chen X., Rolfe A., Halleck A., Hines L., Eisenstein S., Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y., Pielan M., Farmer A.;
RA "Cloning of human full-length cDNAs in BD Creator(TM) System donor vector."
RT Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC002427; AA02427.1; -.
DR EMBL; BT007240; AAP5904.1; -.
DR HSSP; P29466; ITCE.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.

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DR Pfam; PF00656; CARD; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS00209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROTEASE.
SQ SEQUENCE 435 AA; 48869 MW; 10CF5A51F9369E57 CRC64;

Query Match 27.9%; Score 210; DB 4; Length 435;
Best Local Similarity 37.5%; Pred. No. 2.2e-11;
Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;

QY 29 REGSEEDDALAHMFRQLRFESTMKRDPPTARQFOEELKFOQALDSREDPVSCAFVYIMA 88
DB 202 RSGGDVDTHTTIVTLFRLGYNVHVLDQTAQEMQEKLNFAQ-LPAHRTVDSG-VALLS 259
QY 89 HGRGFLKGEDEVKLENTFEALNNKCOALRAKPKYITIOACRGEQDPG 140
DB 260 HGVEGATGVGDKLQLQGVFRLFDNANCPSLQNKPKMFFIOACRGEQDPG 311

RESULT 2
Q8C9H7 PRELIMINARY; PRT; 452 AA.
AC O8C9H7;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Caspase 2.
GN CASP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=2354683; PubMed=12466851;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK042072; BAC31153.1; -.
DR MGD; MGI:97295; Casp2.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS00209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 452 AA; 50689 MW; C3715908508619CA CRC64;

Query Match 27.9%; Score 210; DB 11; Length 452;
Best Local Similarity 38.4%; Pred. No. 2.3e-11;
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Matches 43; Conservative 26; Mismatches 41; Indels 2; Gaps 2;

QY 29 REGSEEDDALAHMFRQLRFESTMKRDPPTARQFOEELKFOQALDSREDPVSCAFVYIMA 88
DB 219 RSGGDVDTHTTIVTLFRLGYNVHVLDQTAQEMQEKLNFAQ-LPAHRTVDSG-VALLS 276
QY 89 HGRGFLKGEDEVKLENTFEALNNKCOALRAKPKYITIOACRGEQDPG 140
DB 277 HGVEGATGVGDKLQLQGVFRLFDNANCPSLQNKPKMFFIOACRGEQDPG 328

RESULT 3
Q8K241 PRELIMINARY; PRT; 452 AA.
AC Q8K241;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Caspase 2.
GN CASP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC034262; AAH34262.1; -.
DR MGD; MGI:97295; Casp2.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS00209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 452 AA; 50661 MW; A4DE25A712FAB855 CRC64;

Query Match 27.5%; Score 207; DB 11; Length 452;
Best Local Similarity 37.5%; Pred. No. 4.4e-11;
Matches 42; Conservative 27; Mismatches 41; Indels 2; Gaps 2;

QY 29 REGSEEDDALAHMFRQLRFESTMKRDPPTARQFOEELKFOQALDSREDPVSCAFVYIMA 88
DB 219 RSGGDVDTHTTIVTLFRLGYNVHVLDQTAQEMQEKLNFAQ-LPAHRTVDSG-VALLS 276
QY 89 HGRGFLKGEDEVKLENTFEALNNKCOALRAKPKYITIOACRGEQDPG 140
DB 277 HGVEGATGVGDKLQLQGVFRLFDNANCPSLQNKPKMFFIOACRGEQDPG 328

RESULT 4
Q85194 PRELIMINARY; PRT; 452 AA.
AC Q85194;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE NEBD2/ICH-1.
OS Rattus norvegicus (Rat).
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98087427; PubMed=9427555;
RA Sato N., Milligan C.E., Uchiyama Y., Oppenheim R.W.,
RT "Cloning and expression of the cDNA encoding rat caspase-2,"
RL Gene 202:127-132(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RA Jin K.U., Simon R.P., Graham S.H.,
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; U77933; AAB96379.1; -.
DR EMBL; AF136231; AAD33684.1; -.
DR PIR; J06507; J06507.
DR HSSP; P29466; 1ICE.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR PRINTS; PR00376; IL1BENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 452 AA; 50728 MW; 03F9D096BB741CE3 CRC64;

Query Match 27.3%; Score 205; DB 11; Length 452;
Best Local Similarity 37.5%; Pred. No. 6,7e-11;
Matches 42; Conservative 21; Mismatches 41; Indels 2; Gaps 2;

QY 29 REGSEEDLDALHEMFQRLRESFMKRDPTAEQFOEELKEKQALDSREDPVSCAFVVLMA 88
Db 219 RSGGDVHTLTVLTLFKLGVNVHVLVDQTQEMQEKLNPAQ-LPAHRTVDS-CVALLS 276
QY 89 HGERGFLKEDGEMVKLENTFEALNNKQCALRAKPKVYITQCRGQRDPG 140
Db 277 HGVGGIYGVGDKLTLQAEVFLFDNANCPSLONKPKMFFIQACRGDETDRG 328

RESULT 5
Q91B63 PRELIMINARY; PRT; 399 AA.
ID Q91B63
AC Q91B63
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Caspase-9.
GN XCASPASE-9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yacita Y.,
RT "Structure, expression and function of the Xenopus laevis caspase
family,"
RL J. Biol. Chem. 275:10484-10491(2000).
J. Biol. Chem. 275:10484-10491(2000).

DR EMBL; AB038172; BAA94750.1; -.
DR HSSP; Q15806; 1ODU.
DR MEROPS; C14.010; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR000488; Death.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
SQ SEQUENCE 399 AA; 44772 MW; EE2A269719064F9F CRC64;

Query Match 27.2%; Score 204.5; DB 13; Length 399;
Best Local Similarity 31.2%; Pred. No. 6,5e-11;
Matches 49; Conservative 26; Mismatches 61; Indels 21; Gaps 4;

QY 2 SNPRSLFEERK-YDMGSAALALILCVT-----KAREGSEEDLDALHEMFQRLRES 50
Db 125 SRKGLDKKKDYPMSSDPIGFCLINNNPHECTGLSTGTSDIDRDLANNRKSHTFEV 184
QY 51 TMKRDPTAEQFOEELKEKQALDSREDPVSCAFVVLMAHGRE-----GFLKGEDGEMV 103
Db 185 TVKDNITGQAMHDHQLALDDQHSLOD-----CCIVLISHGCEHRHIFQGGVYGTGIRI 241

QY 104 KLENTFEALNNKQCALRAKPKVYITQACRGQRDPG 140
Db 242 PVERIVSYFNNGSKPSLRGPKFIITQACGGQDKRG 278

RESULT 6
Q91B67 PRELIMINARY; PRT; 423 AA.
ID Q91B67
AC Q91B67
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Caspase-2.
GN XCASPASE-2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yacita Y.,
RT "Structure, expression and function of the Xenopus laevis caspase
family,"
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL; AB038168; BAA94746.1; -.
DR HSSP; P29466; 1ICE.
DR MEROPS; C14.006; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CARD; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 423 AA; 47123 MW; E91EBFD13FC01FD CRC64;

Query March 26.3%; Score 198; DB 13; Length 423;
Best Local Similarity 35.9%; Pred. No. 2.8e-10;
Matches 42; Conservative 26; Mismatches 37; Indels 12; Gaps 2;

QY 29 REGSEEDLDALHMFRLFEFTMKRDPPTAEQFOELEK-----QQAIDSRDPVSCAF 83
DB 187 RCGGEVDLASLEKLFSSLGVDVRCNLNAGSMSSQLGAFSALPVHSLDS-----CV 239
QY 84 VVLMHGREGLKEDGEMVLENTLEFALNNKNCQALRAKPKVYIIQACRGQDPG 140
DB 240 VVLSHGLDGAIVGTDKLVQLQEVFTALDNHCPQLQNKPKMFFIQACRGEEITDRG 296

RESULT 7
Q86UJ3 PRELIMINARY; PRT; 312 AA.
AC Q86UJ3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein CASP2.
GN CASP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
OC Mammalia; Eutheria; Plimates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99063792; PubMed=9847074;
RA Sulston J.E., Waterston R.;
RT "Toward a complete human genome sequence.";
RL Genome Res. 8:1097-1108 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Doeber A., Martinka S., Maupin R.;
RT "The sequence of Homo sapiens BAC clone RP11-55613.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.H.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC073342; AAP2347.1; -;
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:casepase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001309; ICE_p20.

DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CARD; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hypothetical protein.
SQ SEQUENCE 312 AA; 34866 MW; E518F4B69A7D1414 CRC64;

Query March 26.2%; Score 197; DB 4; Length 312;
Best Local Similarity 37.7%; Pred. No. 2.5e-10;
Matches 40; Conservative 27; Mismatches 37; Indels 2; Gaps 2;

QY 29 REGSEEDLDALHMFRLFEFTMKRDPPTAEQFOELEKFOQAIDSRDPVSCAFVILMA 88
DB 188 RSGGDVHSTLVTLFKLIGDVHVLCDQIAGEMQEKLNFAQ-LPAHRVTDSC-IVALIS 245
QY 89 HGRBGLKEDGEMVLENTLEFALNNKNCQALRAKPKVYIIQACRG 134
DB 246 HGVEGALYGVDKLQLQEVFQLFDNANCPSLQMKPKMFFIQACRG 291

RESULT 8
Q801M6 PRELIMINARY; PRT; 415 AA.
AC Q801M6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049286; AAH49286.1; -;
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:casepase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CARD; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hypothetical protein.
SQ SEQUENCE 415 AA; 46542 MW; CD553432B40BE8B8 CRC64;

Query March 26.1%; Score 196; DB 13; Length 415;
Best Local Similarity 36.6%; Pred. No. 4.2e-10;
Matches 41; Conservative 26; Mismatches 43; Indels 2; Gaps 2;

QY 29 REGSEEDLDALHMFRLFEFTMKRDPPTAEQFOELEKFOQAIDSRDPVSCAFVILMA 88
DB 183 RCGGEVDLASLEKLFSSLGVDVRCNLNAGSMSSQLRAF-SALPVHSLDSCV-VALLIS 240


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DR Pfam; PF00619; CARD; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 393 AA; 42975 MW; CA889475E50DD632 CRC64;

Query Match 25.8%; Score 194; DB 11; Length 393;
Best Local Similarity 37.4%; Pred. No. 6.1e-10;
Matches 46; Conservative 17; Mismatches 42; Indels 18; Gaps 3;

QY 29 REGSEEDLDALAHMFRQLRPESTMKRDPYAEQ----FOELEKFOQALDSREDPVSCAFV 84
DB 218 RTGSNLDKDLKLEHFRFWRFVVEVKNLDTAKKMTALMEMAHRHRAID-----CFVV 270
QY 85 VLMAGRE-----GFLKGEDEGVKLENFELANNKNCQALRAKPKVYITIQACRGEOR 137
DB 271 VILSHGQASHLQPPGAVYGTGCSVSIKLVNIFNSGCGPSLGKPKLFTFIQACGGEQK 330
QY 138 DPG 140
DB 331 DHG 333

RESULT 12
Q8C300 PRELIMINARY; PRT; 453 AA.
ID Q8C300
AC Q8C300;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 9 (Fragment).
GN CASP9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK08152; BAC39378.1; -.
DR MGD; MGI:1277950; Casp9.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
FT NON TER 1
SQ SEQUENCE 453 AA; 49847 MW; 8F7D1C50F7ABA68F CRC64;
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Query Match 25.8%; Score 194; DB 11; Length 454;
Best Local Similarity 37.4%; Pred. No. 7.1e-10;
Matches 46; Conservative 17; Mismatches 42; Indels 18; Gaps 3;

QY 29 REGSEEDLDALAHMFRQLRPESTMKRDPYAEQ----FOELEKFOQALDSREDPVSCAFV 84
DB 217 RTGSNLDKDLKLEHFRFWRFVVEVKNLDTAKKMTALMEMAHRHRAID-----CFVV 269
QY 85 VLMAGRE-----GFLKGEDEGVKLENFELANNKNCQALRAKPKVYITIQACRGEOR 137
DB 270 VILSHGQASHLQPPGAVYGTGCSVSIKLVNIFNSGCGPSLGKPKLFTFIQACGGEQK 329
QY 138 DPG 140
DB 330 DHG 332

RESULT 13
Q9ROT0 PRELIMINARY; PRT; 454 AA.
ID Q9ROT0
AC Q9ROT0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase9.
GN CASP9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2001956; PubMed=10529400;
RA Fujita E., Jinbo A., Matuzaki H., Konishi H., Kikawa U., Momoi T.;
RT "Akt phosphorylation site found in human caspase-9 is absent in mouse
RT caspase-9."
RL Biochem. Biophys. Res. Commun. 264:550-555 (1999).
DR EMBL; AB019600; BAA86895.1; -.
DR PIR; JCT123; JCT123.
DR HSRP; P42574; 1PAU.
DR MEROPS; C14.010; -.
DR MGD; MGI:1277950; Casp9.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR002398; ICE_p20.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 454 AA; 50051 MW; 4614989A7B23850F CRC64;

Query Match 25.8%; Score 194; DB 11; Length 454;
Best Local Similarity 37.4%; Pred. No. 7.2e-10;
Matches 46; Conservative 17; Mismatches 42; Indels 18; Gaps 3;

QY 29 REGSEEDLDALAHMFRQLRPESTMKRDPYAEQ----FOELEKFOQALDSREDPVSCAFV 84
DB 218 RTGSNLDKDLKLEHFRFWRFVVEVKNLDTAKKMTALMEMAHRHRAID-----CFVV 270
QY 85 VLMAGRE-----GFLKGEDEGVKLENFELANNKNCQALRAKPKVYITIQACRGEOR 137
```

Db 271 VILSHGCCASHLQEPGAVYGDGCSVSTIEKIVNIFNNGSGCPSLGKPKLFTIOACGGEOK 330
QY 138 DPG 140
Db 331 DHG 333

RESULT 14

08C309 PRELIMINARY; PRT; 454 AA.
ID 08C309
AC 08C309;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Caspase 9.
GN CASP9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK085095; BAC39365.1; -.
DR MGD; MG1:1277950; Casp9.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILICENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SQUENCE 454 AA; 49979 MW; 438A67EA6A6EE78 CRC64;

Query Match

25.8%; Score 194; DB 11; Length 454;

Best Local Similarity 37.4%; Pred. No. 7.2e-10;
Matches 46; Conservative 17; Mismatches 42; Indels 18; Gaps 3;

QY 29 RRGSEEDLDALHEMFROLPFESTMKRDPPTAEQ---FOEELKFOQAIDSREDPVSCAFV 84
Db 218 RTGSDNDLDRDKLEHFRFWIRFVAVKNDITAKKMTALMEMHRRHRLD-----CFVV 270
QY 85 VLMAGRE-----GFLKGEDGEMVYKLENLFEALNNKNCQALRAKPKVYITIOACRGEOR 137
Db 271 VILSHGCCASHLQEPGAVYGDGCSVSTIEKIVNIFNNGSGCPSLGKPKLFTIOACGGEOK 330
QY 138 DPG 140
Db 331 DHG 333

RESULT 15

Q9WU16 PRELIMINARY; PRT; 343 AA.
ID Q9WU16

AC Q9WU16;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Caspase-25.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Jin K.U., Graham S.H., Simon R.P.;
RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF136232; AAD33685.1; -.
DR HSP; P29466; IICE.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILICENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SQUENCE 343 AA; 38003 MW; 0292D6130C63F641 CRC64;

Query Match

25.5%; Score 192; DB 11; Length 343;

Best Local Similarity 37.7%; Pred. No. 8.1e-10;
Matches 40; Conservative 25; Mismatches 39; Indels 2; Gaps 2;

QY 29 RRGSEEDLDALHEMFROLPFESTMKRDPPTAEQFOEELKFOQAIDSREDPVSCAFVYIMA 88
Db 219 RSGGDVDDHTTVTLVTLFYLGNVHVLYDQTAQEWQEKLNFAQ--LFAHRTVDS-IVALLS 276
QY 89 HGESEGLKGEDGEMVYKLENLFEALNNKNCQALRAKPKVYITIOACRG 134
Db 277 HGEVGGIYGVGDKLQLQEVFRFLPDANCPSLQNKRMFFITIOACRG 322

Search completed: July 12, 2004, 13:50:14

Job time : 29.8636 secs

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: July 12, 2004, 13:39:36 ; Search time 28.562 Seconds
(without alignments)
949.674 Million cell updates/sec

Title: US-10-068-564-5_COPY_147_242
Perfect score: 487
Sequence: 1 EIVWIKDSFGTIPYTDAL.....KARKTNPDIQSTLRRLYLQ 96

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_28Jan04:*

- 1: geneeqp1980s:*
- 2: geneeqp1990s:*
- 3: geneeqp2000s:*
- 4: geneeqp2001s:*
- 5: geneeqp2002s:*
- 6: geneeqp2003as:*
- 7: geneeqp2003bs:*
- 8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	487	100.0	214 3	AAy93216 Amino aci
2	487	100.0	229 3	AAy68865 Amino aci
3	487	100.0	242 3	AAy93214 Amino aci
4	487	100.0	242 5	AAy77980 Full-leng
5	487	100.0	242 5	AAy77984 Full-leng
6	357	73.3	257 3	AAy68864 Amino aci
7	357	73.3	281 2	AAy93592 Mouse cas
8	357	73.3	281 2	AAy93213 Amino aci
9	195	40.0	234 5	AAy72882 Human asp
10	195	40.0	398 5	ABG76499 DNA encod
11	143	29.4	230 3	AAy93215 Amino aci
12	129.5	26.2	503 2	AAy45295 Ced-3 mut
13	129.5	26.2	494 4	ABBB3301 Drosophila
14	127.5	26.2	503 2	AAy45286 Ced-3 mut
15	127.5	26.2	503 2	AAy45304 Ced-3 mut
16	127.5	26.2	503 2	AAy45309 Ced-3 mut
17	127.5	26.2	503 2	AAy45311 Ced-3 mut
18	127.5	26.2	503 2	AAy45292 Ced-3 mut
19	127.5	26.2	503 2	AAy45294 Ced-3 mut
20	127.5	26.2	503 2	AAy45297 Ced-3 mut
21	127.5	26.2	503 2	AAy45317 Ced-3 mut
22	127.5	26.2	503 2	AAy45317 Ced-3 mut
23	127.5	26.2	503 2	AAy45288 Ced-3 mut
24	127.5	26.2	503 2	AAy45290 Ced-3 mut
25	127.5	26.2	503 2	AAy45299 Ced-3 mut

26	127.5	26.2	503 2	AAy45308 Ced-3 mut
27	127.5	26.2	503 2	AAy45314 Ced-3 mut
28	127.5	26.2	503 2	AAy45316 Ced-3 mut
29	127.5	26.2	503 2	AAy45324 Ced-3 mut
30	127.5	26.2	503 2	AAy45278 Ced-3 mut
31	127.5	26.2	503 2	AAy45276 Ced-3 mut
32	127.5	26.2	503 2	AAy45289 Ced-3 mut
33	127.5	26.2	503 2	AAy45291 Ced-3 mut
34	127.5	26.2	503 2	AAy45300 Ced-3 mut
35	127.5	26.2	503 2	AAy45310 Ced-3 mut
36	127.5	26.2	503 2	AAy45293 Ced-3 mut
37	127.5	26.2	503 2	AAy45280 Ced-3 mut
38	127.5	26.2	503 2	AAy45302 Ced-3 mut
39	127.5	26.2	503 2	AAy45303 Ced-3 mut
40	127.5	26.2	503 2	AAy45313 Ced-3 mut
41	127.5	26.2	503 2	AAy45318 Ced-3 mut
42	127.5	26.2	503 2	AAy45281 Ced-3 mut
43	127.5	26.2	503 2	AAy45282 Ced-3 mut
44	127.5	26.2	503 2	AAy45283 Ced-3 mut
45	127.5	26.2	503 2	AAy45287 Ced-3 mut

ALIGNMENTS

RESULT 1
AAy93216
ID AAy93216 standard; protein; 214 AA.
XX
AC AAy93216;
XX
DT 04-SEP-2000 (first entry)
XX
DE Amino acid sequence of a human caspase-14 splice variant.
XX
KW Caspase-14; cell death specific protease; apoptosis stimulator;
XX apoptosis; AIDS; neurodegenerative disease; ischemic injury.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Active-site 102..106
XX
XX WO200028047-A1.
XX
XX 18-MAY-2000.
XX
XX 29-OCT-1999; 99WO-US025523.
XX
XX 06-NOV-1998; 98US-00187789.
XX
XX (UYBE-) UNTIV JEFFERSON THOMAS.
XX
XX Alnemri ES, Fernandez-Alnemri T;
XX WPI, 2000-376558/32.
XX DR N-PSDB; AAA15166.
XX
XX Novel nucleic acids encoding cell death specific protease termed caspase-14 useful for treating cancers by stimulating apoptosis.
XX
XX Claim 42; Fig 9; 78pp; English.
XX
XX The present sequence represents a human caspase-14 splice variant. The
XX polypeptide is a cell death specific protease, and is an apoptosis
XX stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase
XX -14 antibodies are useful for treating or reducing the severity of
XX pathological conditions associated with increased or decreased levels of
XX apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative
XX diseases and ischemic injury are treated by administering anti-caspase-14
XX antibodies. The antibody is useful for determining the presence of the
XX level of caspase-14 in tissue sample and also for the isolation of
XX caspase-14 with apoptotic activity or in screening assay to identify an

CC agent that inhibits heterodimer or heterotetramer formation and
CC therefore, apoptosis
XX
SQ Sequence 214 AA;

Query Match 100.0%; Score 487; DB 3; Length 214;
Best Local Similarity 100.0%; Pred. No. 8.8e-54;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVWVKDSPTPTPTDPAHVSTVSGYIAYRHDDQKSCFIQTLDVDFPKRGHITELL 60
DB 119 EIVWVKDSPTPTPTDPAHVSTVSGYIAYRHDDQKSCFIQTLDVDFPKRGHITELL 178
QY 61 TEVTRMAEAEALVQEGKARKTNPEIOSTLKRILYQ 96
DB 179 TEVTRMAEAEALVQEGKARKTNPEIOSTLKRILYQ 214

RESULT 2

AA68865
ID AAY68865 standard; protein; 229 AA.

AC AAY68865;

DT 16-MAY-2000 (first entry)

DE Amino acid sequence of a human caspase-like polypeptide.

KM Mouse; caspase-like polypeptide; human; caspase; apoptosis; skin disease;
XX keratinisation; wound healing.

OS Homo sapiens.

PN WO200004169-A1.

PD 27-JAN-2000.

PF 12-JUL-1999; 99WO-EP004939.

PR 17-JUL-1998; 98EP-00202422.

PA (VLAAS) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

PI Van De Craen M, Declercq W, Vandenberghe P, Fiers W;

DR WPI: 2000-182433/16.

DR N-PSDB; AA60684.

PT New murine and human caspase homologues useful for treating skin related
XX disorders.

PS Claim 2; Page 53-54; 68pp; English.

XX
CC The present sequence represents a human caspase-like polypeptide. The
CC specification also describes a murine caspase-like polypeptide. Caspases
CC are cysteine/aspartate-specific proteinases which play a central role in
CC apoptosis. The polypeptides of the invention are related to human and
CC murine caspase-2 and human caspase-9, and possess all of the typical
CC amino acids involved in catalysis, including the QACRG box, and contain
CC no or only a very short prodomain. mRNA expression of the homologues of
CC the invention is predominant in the skin. The caspase-like polypeptides
CC are useful for treating human or animal diseases, such as skin diseases.
CC They are also useful for screening for compounds that modulate its
CC activity, i.e. agonists, antagonists, and inhibitors. The caspase-like
CC polypeptides and polynucleotides are useful for modulating
CC keratinisation, for diagnosing and treating inappropriate wound healing
XX

SQ Sequence 229 AA;

Query Match 100.0%; Score 487; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 9.7e-54;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVWVKDSPTPTPTDPAHVSTVSGYIAYRHDDQKSCFIQTLDVDFPKRGHITELL 60
DB 134 EIVWVKDSPTPTPTDPAHVSTVSGYIAYRHDDQKSCFIQTLDVDFPKRGHITELL 193
QY 61 TEVTRMAEAEALVQEGKARKTNPEIOSTLKRILYQ 96
DB 194 TEVTRMAEAEALVQEGKARKTNPEIOSTLKRILYQ 229

RESULT 3

AA93214
ID AAY93214 standard; protein; 242 AA.

AC AAY93214;

DT 04-SEP-2000 (first entry)

DE Amino acid sequence of a human caspase-14.

KM Caspase-14; cell death specific protease; apoptosis stimulator;
XX apoptosis; AIDS; neurodegenerative disease; ischemic injury.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Region 1..146 /note="large subunit"

FT Active-site 130..134

FT Cleavage-site 146..147

FT Region 147..242 /note="small subunit"

PN WO200028047-A1.

PD 18-MAY-2000.

PF 29-OCT-1999; 99WO-US025523.

PR 06-NOV-1998; 98US-00187789.

PA (UYDE-) UNIV JEFFERSON THOMAS.

PI Alnemri ES, Fernandez-Alnemri T;

DR WPI: 2000-376558/32.

DR N-PSDB; AA15164.

PT Novel nucleic acids encoding cell death specific protease termed caspase-
XX 14 useful for treating cancers by stimulating apoptosis.

PS Claim 13; Fig 7; 78pp; English.

XX
CC The present sequence represents a human caspase-14 polypeptide. The
CC polypeptide is a cell death specific protease, and is an apoptosis
CC stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase
CC -14 antibodies are useful for treating or reducing the severity of
CC pathological conditions associated with increased or decreased levels of
CC apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative
CC diseases and ischemic injury are treated by administering anti-caspase-14
CC antibodies. The antibody is useful for determining the presence or the
CC level of caspase-14 in tissue sample and also for the isolation of
CC caspase-14 with apoptotic activity or in screening assay to identify an
CC agent that inhibits heterodimer or heterotetramer formation and
XX therefore, apoptosis

SQ Sequence 242 AA;

Query Match 100.0%; Score 487; DB 3; Length 242;
Best Local Similarity 100.0%; Pred. No. 1e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIVWVKDSPTPTPTDPAHVSTVSGYIAYRHDDQKSCFIQTLDVDFPKRGHITELL 60

Db 147 EIVWVTKDSPTITPTDYLHVSTVEGYIAYRHDKGSCFIOTLVDFVTKRGHILELL 206
QY 61 TEVTRMAAEALVQEGKARKTNPEIOSLTRKRLYLQ 96
Db 207 TEVTRMAAEALVQEGKARKTNPEIOSLTRKRLYLQ 242

RESULT 4
AAG77980
ID AAG77980 standard; protein; 242 AA.

AC AAG77980;

DT 05-APR-2002 (first entry)

DE Full-length human caspase-14.

DE Human; caspase-14; anti-apoptotic; apoptosis.

OS Homo sapiens.

PN W0200181595-A2.

PD 01-NOV-2001.

PF 27-APR-2001; 2001WO-US013831.

PR 27-APR-2000; 2000US-0199962P.

PA (KNOL) KNOLL GMBH.

PI Mankovich JA;

DR WPI; 2002-041410/05.

DR N-PSDB; AAK98248.

PT Novel isolated human caspase-14 proteins and nucleic acid sequences,
PT useful for identifying modulators of caspase-14 protein that are useful
PT for modulating apoptosis.

PS Claim 20; Fig 1; 58pp; English.

CC The sequence represents the novel full-length human caspase-14 protein,
CC referred to as "Caspase-14 NEW" in the specification. The invention
CC relates to a novel isolated human caspase-14 protein comprising an amino
CC acid sequence with MSNPRSLER, at its amino terminus. The caspase-14 of
CC the invention has anti-apoptotic activity. Caspase-14 acts as a modulator
CC of caspase-14 activity. The polypeptide is useful for identifying a
CC compound which is a modulator of human caspase-14 activity, and is also
CC useful for identifying a target molecule. An antibody to caspase-14 is useful
CC for isolating the protein by standard techniques, and for detecting
CC for isolating the protein by standard techniques, and for detecting
CC caspase-14 to evaluate the abundance and expression pattern. The antibody
CC is also useful for diagnostically monitoring protein levels in a tissue
CC as a part of a clinical testing procedure. The polypeptide is useful as a
CC protease to cleave substrates and for inducing apoptosis in cells, in
CC screening assays, and as a bait protein in a two-hybrid or three-hybrid
CC assay to identify other proteins that interact with human caspase-14
CC protein

XX Sequence 242 AA;

XX Query Match 100.0%; Score 487; DB 5; Length 242;

XX Best Local Similarity 100.0%; Pred. No. 1e-53;

XX Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVWVTKDSPTITPTDYLHVSTVEGYIAYRHDKGSCFIOTLVDFVTKRGHILELL 60

Db 147 EIVWVTKDSPTITPTDYLHVSTVEGYIAYRHDKGSCFIOTLVDFVTKRGHILELL 206

QY 61 TEVTRMAAEALVQEGKARKTNPEIOSLTRKRLYLQ 96

Db 207 TEVTRMAAEALVQEGKARKTNPEIOSLTRKRLYLQ 242

RESULT 5
AAG77984
ID AAG77984 standard; protein; 242 AA.

AC AAG77984;

DT 05-APR-2002 (first entry)

DE Full-length human caspase-14 old.

DE Human; caspase-14; anti-apoptotic; apoptosis.

OS Homo sapiens.

PN W0200181595-A2.

PD 01-NOV-2001.

PF 27-APR-2001; 2001WO-US013831.

PR 27-APR-2000; 2000US-0199962P.

PA (KNOL) KNOLL GMBH.

PI Mankovich JA;

DR WPI; 2002-041410/05.

PT Novel isolated human caspase-14 proteins and nucleic acid sequences,
PT useful for identifying modulators of caspase-14 protein that are useful
PT for modulating apoptosis.

PS Example; Fig 1; 58pp; English.

CC The sequence represents the full-length human caspase-14 protein,
CC referred to as "Caspase-14 OLD" in the specification. The invention
CC relates to a novel isolated human caspase-14 protein comprising an amino
CC acid sequence with MSNPRSLER, at its amino terminus. The caspase-14 of
CC the invention has anti-apoptotic activity. Caspase-14 acts as a modulator
CC of caspase-14 activity. The polypeptide is useful for identifying a
CC compound which is a modulator of human caspase-14 activity, and is also
CC useful for identifying a compound which modulates the interaction of
CC caspase-14 with a target molecule. An antibody to caspase-14 is useful
CC for isolating the protein by standard techniques, and for detecting
CC for isolating the protein by standard techniques, and for detecting
CC caspase-14 to evaluate the abundance and expression pattern. The antibody
CC is also useful for diagnostically monitoring protein levels in a tissue
CC as a part of a clinical testing procedure. The polypeptide is useful as a
CC protease to cleave substrates and for inducing apoptosis in cells, in
CC screening assays, and as a bait protein in a two-hybrid or three-hybrid
CC assay to identify other proteins that interact with human caspase-14
CC protein

XX Sequence 242 AA;

XX Query Match 100.0%; Score 487; DB 5; Length 242;

XX Best Local Similarity 100.0%; Pred. No. 1e-53; Indels 0; Gaps 0;

XX Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVWVTKDSPTITPTDYLHVSTVEGYIAYRHDKGSCFIOTLVDFVTKRGHILELL 60

Db 147 EIVWVTKDSPTITPTDYLHVSTVEGYIAYRHDKGSCFIOTLVDFVTKRGHILELL 206

QY 61 TEVTRMAAEALVQEGKARKTNPEIOSLTRKRLYLQ 96

Db 207 TEVTRMAAEALVQEGKARKTNPEIOSLTRKRLYLQ 242

RESULT 6

AA568864

Id AAY68864 standard; protein; 257 AA.

XX

```

AC  AAY68864;
XX
DT  16-MAY-2000 (first entry)
XX
DE  Amino acid sequence of a murine caspase-like polypeptide.
XX
KW  Mouse; caspase-like polypeptide; human; caspase; apoptosis; skin disease;
XX  keratinisation; wound healing.
XX
OS  Mus musculus.
XX
PN  WO200004169-A1.
XX
PD  27-JAN-2000.
XX
PF  12-UTL-1999; 99WO-EP004939.
XX
PR  17-JUL-1998; 98EP-00202422.
XX
PA  (VLA-) VLAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI  Van De Craen M, Declercq W, Vandenaebroe P, Piers W;
XX  WPI; 2000-182433/16.
XX  DR  N-PSDB; AAZ60683.
XX
PT  New murine and human caspase homologues useful for treating skin related
PT  disorders.
XX
PS  Claim 1; Page 51-52; 68pp; English.
XX
CC  The present sequence represents a murine caspase-like polypeptide. The
CC  specification also describes a human caspase-like polypeptide. Caspases
CC  are cysteinyl aspartate-specific proteinases which play a central role in
CC  apoptosis. The polypeptides of the invention are related to human and
CC  murine caspase-2 and human caspase-9, and possess all of the typical
CC  amino acids involved in catalysis, including the QACRQ box, and contain
CC  not only a very short prodomain. mRNA expression of the homologues of
CC  the invention is predominant in the skin. The caspase-like polypeptides
CC  are useful for treating human or animal diseases, such as skin diseases.
CC  They are also useful for screening for compounds that modulate its
CC  activity, i.e. agonists, antagonists, and inhibitors. The caspase-like
CC  polypeptides and polynucleotides are useful for modulating the
CC  keratinisation, for diagnosing and treating inappropriate wound healing
XX
SQ  Sequence 257 AA;
XX
Query Match 73.3%; Score 357; DB 3; Length 257;
Best Local Similarity 70.2%; Pred No. 5.4e-37;
Matches 66; Conservative 14; Mismatches 14; Indels 0; Gaps 0;
OY 3 VMTKDSQPTITPTTDTALHVSSTVEGYIAYRDQKSGCIQTLDVFTFRKSHLELTE 62
DB 164 VAVLNPNQPSIPTVYDTHIYSTVGVLSTYRDEKSGEIQTLVDVFIHKKSIIELTBE 223
OY 63 VTRRMAEALVQEGARKTNPEIQSTLAKRLYLQ 96
DB 224 ITRLMANTVEWQEGPKRVNPEVOSTLRKKYLQ 257
XX
RESULT 7
XX  ID AAW93592 standard; protein; 281 AA.
XX  AAW93592;
XX  AAW93592;
XX  21-JUN-1999 (first entry)
XX
DE  Mouse caspase-14 protein.
XX
KW  Caspase-14; murine; protease; treatment; apoptotic-related disease;
XX  autoimmune disease; cancer; acquired immunodeficiency syndrome; AIDS;
XX  neurodegenerative disease; ischaemic injury; anti-idiotypic antibody;

```

XX	caspase-14 processing activity; epitope; competitor; modulator.
OS	Mus sp.
PN	WO910504-A2.
PP	04-MAR-1999.
XX	
XX	26-ATG-1998; 98WO-US017715.
PF	26-ATG-1997; 97US-0056986P.
XX	
PA	(IDUN-) IDUN PHARM INC.
XX	
PI	Alnemri ES, Fernandes-Alnemri T;
DR	WPI, 1999-204670/17.
XX	N-FSDB; AAX23515.
PT	Newly isolated polynucleotide encoding a caspase-14 polypeptide - useful
PR	for identifying (ant)agonists that are useful in the diagnosis and
XX	treatment of apoptosis-related diseases.
PS	Claim 4, Fig 1; 5pp; English.
XX	
CC	This invention describes a novel murine caspase-14 which has protease
CC	activity. The caspase-14 polypeptide is useful for identifying
CC	(ant)agonists of the polypeptide, where enzyme activity is measured with
CC	a fluorescent substrate (especially DEVD-AMC or YVAD-AMC. Activated
CC	caspase-14 is useful for identifying inhibitors or enhancers of caspase-
CC	14 activity. The compounds identified by both methods form pharmaceutical
CC	compositions for treating apoptotic-related diseases, including
CC	autoimmune disease, cancer, acquired immunodeficiency syndrome (AIDS),
CC	neurodegenerative diseases and ischemic injury. The anti-caspase-14
CC	antibody is useful for measuring the level of caspase-14 in a tissue
CC	sample. An antibody that binds to a caspase-14 polypeptide is useful for
CC	isolating the polypeptide, and an antibody that binds to the large or
CC	small subunit the polypeptide is useful for identifying samples with
CC	caspase-14 processing activity. An antibody that binds to caspase-14
CC	heterodimer or heterotetramer is useful for isolating caspase-14 with
CC	apoptotic activity or in a screening assay to identify (ant)agonists. The
CC	antibodies form kits for such purposes. The anti-caspase-14 antibody is
CC	also useful for preparing anti-idiotypic antibodies, which mimic a
CC	caspase-14 epitope recognized by the anti-caspase-14 antibody. Therefore,
CC	the antibody is useful as a competitor of caspase-14 in reducing the
CC	level of caspase-14 activity, which reduces the level of apoptotic
CC	activity. Oligonucleotides made from the polynucleotides are useful as
CC	polymerase chain reaction (PCR) primers or probes to screen genomic or
CC	CDNA libraries for similar caspase-14 encoding polynucleotides, or for
CC	diagnosis of diseases associated with enhanced or inhibited apoptosis.
CC	The isolated caspase-14 gene permits methods of modulating apoptosis for
CC	the treatment of human diseases
XX	
XX	Sequence 281 AA;
SQ	
Query Match	73.3%; Score 357; DB 2; Length 281;
Best local Similarity	70.2%; Pred. No. 6.1e-37;
Matches	66; Conservative 14; Mismatches 14; Indels 0; Gaps 0;
Oy	3 VMTKDSPOLITPYTDALAHVSTVEGVYAYRHDKSGSCFIOTLWVFETXKRKHILELTE 62 ::: ::: ::: :::
Db	183 VAVLKNNNPQSIPYTTDLHIHISTYBGLVSYNHDEKSGSFIOITLDVFIHKGSIIIELTBE 242 ::: ::: ::: :::
Oy	63 VTRMAEHLVQEGKARKTNPEIQTSTRKLILYLQ 96 ::: ::: ::: :::
Db	243 ITRLMANTEVQEGKPKRVNPEVOSTLRKKLYLQ 276 ::: ::: ::: :::
RESULT 8	
ID	AAY93213 standard; protein; 281 AA.
XX	
GC	AAY93213;

XX 04-SEP-2000 (first entry)
XX Amino acid sequence of a murine caspase-14.
DE Caspase-14, cell death specific protease; apoptosis stimulator;
KW apoptosis; AIDS; neurodegenerative disease; ischemic injury.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FH Region 1..156
FT /note="large subunit"
FT Active-site 134..138
FT Cleavage-site 156..157
FT Cleavage-site 162..163
FT Region 163..257
FT /note="small subunit"
XX
PN WO200028047-A1.
XX
PD 18-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US025523.
XX
PR 06-NOV-1998; 98US-00187789.
XX
PA (UYJE-) UNITV JEFFERSON THOMAS.
XX
PI Alnemri ES, Fernandez-Alnemri T;
XX
PI WPI, 2000-376558/32.
XX
DR N-PSDB; AAA15163.
XX
PT Novel nucleic acids encoding cell death specific protease termed caspase-
PT 14 useful for treating cancers by stimulating apoptosis.
XX
PS Claim 52; Fig 1; 78pp; English.
XX
XX The present sequence represents a murine caspase-14 polypeptide. The
XX polypeptide is a cell death specific protease, and is an apoptosis
XX stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase
XX -14 antibodies are useful for treating or reducing the severity of
XX pathological conditions associated with increased or decreased levels of
XX apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative
XX diseases and ischemic injury are treated by administering anti-caspase-14
XX antibodies. The antibody is useful for determining the presence or the
XX level of caspase-14 in tissue sample and also for the isolation of
XX caspase-14 with apoptotic activity or in screening assay to identify an
XX agent that inhibits heterodimer or heterotetramer formation and
XX therefore, apoptosis
XX
SQ Sequence 281 AA;
Query Match 73.3%; Score 357; DB 3; Length 281;
Best Local Similarity 70.2%; Pred. No. 6.1e-37;
Matches 66; Conservative 14; Mismatches 14; Indels 0; Gaps 0;
QY 3 VMTYKSPQITPTTALHYSTVEGYIAYRHDKSGSCFIQTLDVDFTRKKGHILELTLTE 62
DB 183 VAVYKNNPQSIPTTDLIHYSTVEGYLSTRHDEKSGFIQTLDVDFTRKKGHILELTLTE 242
QY 63 VTRRMAELVQSGKARKNPETIOSTLRKRLYLQ 96
DB 243 ITRLMANTEVWQSGKPRKVNPEVOSTLRKRLYLQ 276
RESULT 9
AAU72882
ID AAU72882 standard; protein; 234 AA.
XX
AC AAU72882;
XX

DT 26-FEB-2002 (first entry)
DE Human aspartyl protease partial protein sequence #7.
XX
XX Human; protease; PCR primer; cytosolic; immunomodulator; cardiant;
KW vasotropic; antihypertensive; analgesic; endocrine; nootropic; tranquilizer;
KW hypertensive; hypotensive; neuroleptic; neuroprotective; anabolic;
KW anorectic; antiinflammatory; aspartyl protease; cysteine protease;
KW metalloprotease; serine protease; cancer; hematopoietic; breast; colon;
KW lung; prostate; cervical; brain; ovarian; bladder; kidney; pain;
KW immune-related disease; cardiovascular disease; neuronal disease;
KW migraine; sexual dysfunction; mood disorder; attention disorder;
KW cognition disorder; hypertension; hypertensive; psychotic disorder;
KW dyslexia; metabolic disorder; inflammatory disorder.
XX
OS Homo sapiens.
XX
PN WO200183782-A2.
XX
PD 08-NOV-2001.
XX
PF 04-MAY-2001; 2001WO-US014431.
XX
PR 04-MAY-2000; 2000US-0201879P.
XX
PA (SUGJ-) SUGEN INC.
XX
PI Plowman GD, Whyte D, Sudarsanam S, Manning G, Caenepeel S;
PI Payne V;
XX
PI WPI; 2002-041502/05.
XX
DR N-PSDB; AAS97165.
XX
PT Novel protease polypeptide useful for screening for substances that may
PT be used to treat, e.g., cancers, immune-related diseases, cardiovascular
PT disease, migraine, pain, psychotic and inflammatory disorders.
XX
PS Claim 28; Fig 2A; 232pp; English.
XX
XX The invention relates to an isolated, enriched, or purified protease
XX polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to
XX screen for substances (S) that may modulate its activity. Administering S
XX (which modulates protease activity in vitro) may be used to treat a
XX disease or disorder selected from cancers (e.g., of tissues, of blood or
XX hematopoietic origin, of the breast, colon, lung, prostate, cervical,
XX brain, ovarian, bladder or kidney), immune-related diseases and diseases
XX of disorders, cardiovascular disease, brain or neuronal-associated diseases
XX (e.g., central or peripheral nervous system diseases, migraine, pain,
XX sexual dysfunction, mood disorders, attention disorders, cognition
XX disorders, hypertension, hypertensive, psychotic disorders, neurological
XX disorders and dyslexia), metabolic disorders and inflammatory
XX disorders. (I) may also be useful as a diagnostic tool for a disease or
XX disorder such as those above. AAU72876-AAU72910 represent human protease
XX amino acid sequences of the invention
XX
SQ Sequence 234 AA;
Query Match 40.0%; Score 195; DB 5; Length 234;
Best Local Similarity 48.4%; Pred. No. 2.9e-16;
Matches 44; Conservative 18; Mismatches 25; Indels 4; Gaps 3;
QY 9 SPQITPTTALHYSTVEGYIAYRHDKSGSCFIQTLDVDFTRKKGH-ILELTVYRRM 67
DB 144 APSPVSHADVQIYVAQGYVVR-DDKQSDPIQTIVELVRANPGHDLLELTVYRRV 202
QY 68 AEAELVQE--GKARKNPETIOSTLRKRLYLQ 96
DB 203 CEQGVIGPDDDELKAKCTLRSSLRRLRLCQ 233
RESULT 10
ABG76499
ID ABG76499 standard; protein; 398 AA.
XX

Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVWIKDSPQTIPTTYDALHYSTVEG 28
147 EIVWIKDSPQTIPTTYDALHYSTVEG 174

RESULT 12

AA045325
ID AA045325 standard; protein; 503 AA.

AC AA045325;

DT 25-MAR-2003 (revised)
DT 01-JUL-1994 (first entry)

DE Ced-3 mutant V452.

KM C.elegans; cell death; gene; ced-3; inhibition; human; parasite;
KM interleukin-1beta convertase; ICE; pro-interleukin-1beta; cytokine;
KM inflammatory response; nematode; diagnosis; myocardial infarction;
KM stroke; degenerative disease; traumatic brain injury; hypoxia; pest;
KM pathogenic infection; hair loss; cancer; autoreactive antibody.

OS Caenorhabditis elegans.

FH Key Location/Qualifiers

FT Misc-difference 452
FT /label= V452

PN WO9325694-A1.

PD 23-DEC-1993.

PF 14-JUN-1993; 93WO-US005705.

PR 12-JUN-1992; 92US-00897786.

PR 20-NOV-1992; 92US-00984182.

PA (MAST) MASSACHUSETTS INST TECHNOLOGY.

PI Horvitz HR, Yuan J, Shaham S;

DR WPI; 1994-007551/01.

PT Agents which affect activity of cell death genes - used to develop drugs
PT for treating conditions characterised by cell death or proliferation.

PS Claim 99; Page 7; 132pp; English.

CC The sequences given in AA045276-328 indicate the positions of possible
CC mutations of the C.elegans cell death gene, ced-3. These mutations occur
CC at conserved amino acid residues of the Ced-3 protein. Fragments of the
CC amino terminal of these proteins act as inhibitors of Ced-3. The ced-3
CC gene has considerable similarity to human interleukin-1beta convertase
CC (ICE), which converts pro-interleukin-1beta to the active cytokine and is
CC involved in inflammatory response in humans. The similarity between the
CC two sequences suggests that inhibitors of ced-3 may also act as
CC inhibitors of ICE. Human ICE and nematode Ced-3 proteins have an overall
CC amino acid similarity of 28%. The ced-3 inhibitors may be used for
CC identifying agents which affect the activity of a gene belonging to the
CC to the ced-3/ICE family of genes and for diagnosis of diseases
CC characterised by cell death. They can also be used to develop drugs for
CC treating conditions characterised by cell deaths such as myocardial
CC infarction, stroke, degenerative disease, traumatic brain injury,
CC hypoxia, pathogenic infection, or hair loss, or drugs for reducing the
CC proliferative capacity or size of a population of cells such as cancerous
CC cells, cells which produce autoreactive antibodies, infected cells, hair
CC follicle cells or cells which are critical to the life of a parasite,
CC pest or recombinant organism. They may also be used in the diagnosis of
CC inflammatory disease. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 503 AA;

Query Match 26.6%; Score 129.5; DB 2; Length 503;

Best Local Similarity 35.7%; Pred. No. 2.1e-07;
Matches 30; Conservative 19; Mismatches 32; Indels 3; Gaps 2;

Qy 14 PTYDALHYSTVEGYIARHDKGSCPIQTLVVFET--KRGHILELTETVRMAAE 71
410 PSQADILIRYATITQYVSRNSARSGWFIQVCEVFTHADXDVEVLTETVKNKVASAF 469

Qy 72 LVQEG-KARKTNPEIQTSLRRRLY 94

DB 470 QTSQGSNTLKMPEMSTRLLKKFY 493

RESULT 13

ABB63301
ID ABB63301 standard; protein; 494 AA.

AC ABB63301;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 16695.

KM Drosophila; developmental biology; cell signalling; insecticide;
KM pharmaceutical.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US009231.

PR 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

PA (PERK) PE CORP NY.

PI Venter JC, Adams M, Li PMD, Myers EW;

DR WPI; 2001-656860/75.

DR N-PSDB; ABL07404.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.

PS Disclosure; SEQ ID NO 16695; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

CC Sequence 494 AA;

Query Match 26.2%; Score 127.5; DB 4; Length 494;

Best Local Similarity 37.2%; Pred. No. 3.7e-07;
Matches 32; Conservative 12; Mismatches 27; Indels 15; Gaps 3;

Qy 16 YTDALHYSTVEGYIARHDKGSCPIQTLVVFTRKG--HILELTETVRMAAE 73
412 HIDMLRMSYTVAGYALRHTQTGSGWFIQVCEVFTHADXDVEVLTETVKNKVASAF 466

QY 74 QEGKARKTN-----PEIQSTLRKRLY 94
 Db 467 ---KKRGSNDSEWPNVKSTFRQHVY 489

RESULT 14
 AAR45286

ID AAR45286 standard; protein; 503 AA.

AC AAR45286;

DT 25-MAR-2003 (revised)

DT 01-JUL-1994 (first entry)

DE Ced-3 mutant D265.

XX C.elegans; cell death; gene; ced-3; inhibition; human; parasite;
 KM interleukin-1beta convertase; ICE; pro-interleukin-1beta; cytokine;
 KM inflammatory response; nematode; diagnosis; myocardial infarction;
 KM stroke; degenerative disease; traumatic brain injury; hypoxia; pest;
 KM pathogenic infection; hair loss; cancer; autoreactive antibody.

OS Caenorhabditis elegans.

EH Key Location/Qualifiers
 FT Misc-difference 265
 FT /label= D265

PN W09325694-A1.

XX 23-DEC-1993.

PD 14-JUN-1993; 93WO-US005705.

PR 12-JUN-1992; 92US-00897788.
 PR 20-NOV-1992; 92US-00984182.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

PI Horvitz HR, Yuan J, Shaham S;

XX WPI; 1994-007551/01.

Agents which affect activity of cell death genes - used to develop drugs
 for treating conditions characterised by cell death or proliferation.

PS Claim 99; Page ?; 132pp; English.

XX The sequences given in AAR45276-328 indicate the positions of possible
 CC mutations of the C.elegans cell death gene, ced-3. These mutations occur
 CC at conserved amino acid residues of the Ced-3 protein. Fragments of the
 CC amino terminal of these proteins act as inhibitors of Ced-3. The ced-3
 CC gene has considerable similarity to human interleukin-1beta convertase
 CC (ICE), which converts pro-interleukin-1beta to the active cytokine and is
 CC involved in inflammatory response in humans. The similarity between the
 CC two sequences suggests that inhibitors of ced-3 may also act as
 CC inhibitors of ICE. Human ICE and nematode Ced-3 proteins have an overall
 CC amino acid similarity of 28%. The ced-3 inhibitors may be used for
 CC identifying agents which affect the activity of a gene belonging to the
 CC to the ced-3/ICE family of genes and for diagnosis of diseases
 CC characterised by cell death. They can also be used to develop drugs for
 CC treating conditions characterised by cell deaths such as myocardial
 CC infarction, stroke, degenerative disease, traumatic brain injury,
 CC hypoxia, pathogenic infection, or hair loss; or drugs for reducing the
 CC proliferative capacity or size of a population of cells such as cancerous
 CC cells, cells which produce autoreactive antibodies, infected cells, hair
 CC follicle cells or cells which are critical to the life of a parasite,
 CC pest or recombinant organism. They may also be used in the diagnosis of
 CC inflammatory disease. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 503 AA;

Query Match

26.2%; Score 127.5; DB 2; Length 503;

Best Local Similarity 35.7%; Pred. No. 3.8e-07;
 Matches 30; Conservative 19; Mismatches 32; Indels 3; Gaps 2;

QY 14 PLYTDLHVYSTEVEGYIAYRHDKGSCFIQTLDVDF--RRKGHIELTEVRMAAE 71
 Db 410 PSQADILIRATYTAQYVSWNSARGSWFIQAVCEVSTHAKMDVVELTEVKRYASAP 469

QY 72 LVQEG-KARKTPEIQSTLRKRLY 94
 Db 470 QTSQGSNIIKQMEPMTSRLLKPFY 493

RESULT 15

AAR45304
 ID AAR45304 standard; protein; 503 AA.

AC AAR45304;

DT 25-MAR-2003 (revised)

DT 01-JUL-1994 (first entry)

DE Ced-3 mutant I321.

XX C.elegans; cell death; gene; ced-3; inhibition; human; parasite;
 KM interleukin-1beta convertase; ICE; pro-interleukin-1beta; cytokine;
 KM inflammatory response; nematode; diagnosis; myocardial infarction;
 KM stroke; degenerative disease; traumatic brain injury; hypoxia; pest;
 KM pathogenic infection; hair loss; cancer; autoreactive antibody.

OS Caenorhabditis elegans.

EH Key Location/Qualifiers
 FT Misc-difference 321
 FT /label= I321

PN W09325694-A1.

XX 23-DEC-1993.

PD 14-JUN-1993; 93WO-US005705.

PR 12-JUN-1992; 92US-00897788.
 PR 20-NOV-1992; 92US-00984182.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

PI Horvitz HR, Yuan J, Shaham S;

XX WPI; 1994-007551/01.

Agents which affect activity of cell death genes - used to develop drugs
 for treating conditions characterised by cell death or proliferation.

PS Claim 99; Page ?; 132pp; English.

XX The sequences given in AAR45276-328 indicate the positions of possible
 CC mutations of the C.elegans cell death gene, ced-3. These mutations occur
 CC at conserved amino acid residues of the Ced-3 protein. Fragments of the
 CC amino terminal of these proteins act as inhibitors of Ced-3. The ced-3
 CC gene has considerable similarity to human interleukin-1beta convertase
 CC (ICE), which converts pro-interleukin-1beta to the active cytokine and is
 CC involved in inflammatory response in humans. The similarity between the
 CC two sequences suggests that inhibitors of ced-3 may also act as
 CC inhibitors of ICE. Human ICE and nematode Ced-3 proteins have an overall
 CC amino acid similarity of 28%. The ced-3 inhibitors may be used for
 CC identifying agents which affect the activity of a gene belonging to the
 CC to the ced-3/ICE family of genes and for diagnosis of diseases
 CC characterised by cell death. They can also be used to develop drugs for
 CC treating conditions characterised by cell deaths such as myocardial
 CC infarction, stroke, degenerative disease, traumatic brain injury,
 CC hypoxia, pathogenic infection, or hair loss; or drugs for reducing the
 CC proliferative capacity or size of a population of cells such as cancerous
 CC cells, cells which produce autoreactive antibodies, infected cells, hair

CC follicle cells or cells which are critical to the life of a parasite,
 CC pest or recombinant organism. They may also be used in the diagnosis of
 CC inflammatory disease. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 503 AA;

Query Match 26.2%; Score 127.5; DB 2; Length 503;
 Best Local Similarity 35.7%; Pred. No. 3.8e-07;
 Matches 30; Conservative 19; Mismatches 32; Indels 3; Gaps 2;
 QY 14 PLYTDALHVSSTVEGYIAVRHDGKSCFIQTLVDVFT--KRGHILELLEVTTRMAEAE 71
 Db 410 PSQADILIRYATTAQYVSMRNSARGSWFIQAVCEVFTSHAKMDVVELLEVNKKVASAF 469
 QY 72 LVQEG-KAKTNPEIQSTLRKRLY 94
 Db 470 QTSQGSNLIKQPEMTSRLKKFY 493

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 Job time : 29.562 secs

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Run on: July 12, 2004, 13:45:17 ; Search time 8.33058 Seconds

(without alignments)
594.928 Million cell updates/sec

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Perfect score: 487
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Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	487	100.0	214	4	US-09-187-789-9 Sequence 9, Appli
2	487	100.0	242	4	US-09-187-789-5 Sequence 5, Appli
3	357	73.3	260	4	US-09-187-789-2 Sequence 2, Appli
4	357	73.3	260	4	US-09-139-600-2 Sequence 2, Appli
5	204	41.9	53	4	US-09-187-789-65 Sequence 65, Appli
6	204	41.9	53	4	US-09-139-600-60 Sequence 60, Appli
7	143	23.4	230	4	US-09-187-789-7 Sequence 7, Appli
8	123.5	25.4	497	2	US-08-394-189B-6 Sequence 6, Appli
9	123.5	25.4	497	3	US-08-258-287B-37 Sequence 37, Appli
10	123.5	25.4	497	3	US-08-368-704C-37 Sequence 37, Appli
11	123.5	25.4	503	3	US-08-258-287B-36 Sequence 36, Appli
12	123.5	25.4	503	3	US-08-368-704C-36 Sequence 36, Appli
13	123.5	25.4	505	2	US-08-394-189B-5 Sequence 5, Appli
14	123.5	25.4	505	2	PCT-US93-05701-20 Sequence 20, Appli
15	123.5	25.4	505	5	PCT-US93-05701-5 Sequence 5, Appli
16	122.5	25.2	503	4	US-09-291-288-12 Sequence 12, Appli
17	119.5	24.5	489	4	US-08-983-502-9 Sequence 9, Appli
18	119.5	24.5	489	4	US-09-516-747-9 Sequence 9, Appli
19	119.5	24.5	489	5	PCT-US96-10521-9 Sequence 9, Appli
20	119.5	24.5	503	3	US-08-258-287B-2 Sequence 2, Appli
21	119.5	24.5	503	3	US-08-258-287B-35 Sequence 35, Appli
22	119.5	24.5	503	3	US-08-368-704C-2 Sequence 2, Appli
23	119.5	24.5	503	3	US-08-368-704C-35 Sequence 35, Appli
24	119.5	24.5	503	4	US-08-724-378D-10 Sequence 10, Appli
25	119.5	24.5	503	5	PCT-US93-05701-19 Sequence 19, Appli
26	119.5	24.5	503	5	PCT-US93-05705-2 Sequence 2, Appli
27	119	24.4	277	2	US-08-890-542A-2 Sequence 2, Appli

28	117.5	24.1	480	5	PCT-US93-05701-21 Sequence 21, Appli
29	117.5	24.1	480	5	PCT-US93-05705-6 Sequence 6, Appli
30	113	23.2	346	2	US-08-618-408B-2 Sequence 2, Appli
31	113	23.2	389	4	US-08-724-378D-2 Sequence 2, Appli
32	113	23.2	389	4	US-08-724-378D-3 Sequence 3, Appli
33	113	23.2	479	1	US-08-665-220-2 Sequence 2, Appli
34	113	23.2	479	3	US-09-291-692-2 Sequence 2, Appli
35	113	23.2	479	4	US-09-561-756-33 Sequence 33, Appli
36	113	23.2	479	4	US-09-227-721-33 Sequence 33, Appli
37	113	23.2	479	4	US-09-954-697-33 Sequence 33, Appli
38	113	23.2	479	4	US-09-009-893A-4 Sequence 4, Appli
39	113	23.2	479	4	US-09-489-155-4 Sequence 4, Appli
40	110	22.6	277	3	US-08-591-605-2 Sequence 2, Appli
41	110	22.6	277	3	US-08-964-308-6 Sequence 6, Appli
42	110	22.6	277	3	US-08-964-308-10 Sequence 10, Appli
43	110	22.6	277	3	US-08-462-969B-4 Sequence 4, Appli
44	110	22.6	277	3	US-08-964-313-6 Sequence 6, Appli
45	110	22.6	277	3	US-08-964-313-10 Sequence 10, Appli

ALIGNMENTS

```
RESULT 1
US-09-187-789-9
; Sequence 9, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemuri, Emad S.
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-187-789-9

Query Match      100.0%; Score 487; DB 4; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.8e-56;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q1 1 EIVWIKSPQITPTTDLHVSTVEGYIVRHQKSCFTQTLVDVETKRGHILEL 60
   |||
Db 119 EIVWIKSPQITPTTDLHVSTVEGYIVRHQKSCFTQTLVDVETKRGHILEL 178
   |||

Q1 61 TEVTRMAEAEIVQKARKTNPEIQSTLRKRLYLQ 96
   |||
Db 179 TEVTRMAEAEIVQKARKTNPEIQSTLRKRLYLQ 214
   |||

RESULT 2
US-09-187-789-5
; Sequence 5, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemuri, Emad S.
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 242
; TYPE: PRT
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```

; ORGANISM: Homo sapien
US-09-187-789-5

Query Match
Best Local Similarity 100.0%; Score 487; DB 4; Length 242;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVWYIKDSPTIPTYTDALHVSTVEGYIAYRHDKSGSCFIQTLVDVFTKRKHILELL 60
DB 147 EVWYIKDSPTIPTYTDALHVSTVEGYIAYRHDKSGSCFIQTLVDVFTKRKHILELL 206

QY 61 TEVTRMAEAEVQEGKARKTNPEIQSTLRKRLYLQ 96
DB 207 TEVTRMAEAEVQEGKARKTNPEIQSTLRKRLYLQ 242

RESULT 3
US-09-187-789-2
; Sequence 2, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-2

Query Match
Best Local Similarity 73.3%; Score 357; DB 4; Length 260;
Matches 66; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 3 VVWIKDSPTIPTYTDALHVSTVEGYIAYRHDKSGSCFIQTLVDVFTKRKHILELL 62
DB 167 VAVLKNPQSIPTIPTYTDALHVSTVEGYIAYRHDKSGSCFIQTLVDVFTKRKHILELL 226

QY 63 VTRMAEAEVQEGKARKTNPEIQSTLRKRLYLQ 96
DB 227 ITRMANTEVMQEGKARKTNPEIQSTLRKRLYLQ 260

RESULT 4
US-09-139-600-2
; Sequence 2, Application US/09139600
; Patent No. 6432628
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHOD OF USE
; FILE REFERENCE: 480140.434
; CURRENT APPLICATION NUMBER: US/09/139,600
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-2

Query Match
Best Local Similarity 73.3%; Score 357; DB 4; Length 260;
Matches 66; Conservative 14; Mismatches 14; Indels 0; Gaps 0;
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```

QY 3 VVWIKDSPTIPTYTDALHVSTVEGYIAYRHDKSGSCFIQTLVDVFTKRKHILELL 62
DB 167 VAVLKNPQSIPTIPTYTDALHVSTVEGYIAYRHDKSGSCFIQTLVDVFTKRKHILELL 226

QY 63 VTRMAEAEVQEGKARKTNPEIQSTLRKRLYLQ 96
DB 227 ITRMANTEVMQEGKARKTNPEIQSTLRKRLYLQ 260

RESULT 5
US-09-187-789-65
; Sequence 65, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 65
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-65

Query Match
Best Local Similarity 41.9%; Score 204; DB 4; Length 53;
Matches 36; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 3 VVWIKDSPTIPTYTDALHVSTVEGYIAYRHDKSGSCFIQTLVDVFTKRKHILELL 53
DB 3 VAVLKNPQSIPTIPTYTDALHVSTVEGYIAYRHDKSGSCFIQTLVDVFTKRKHILELL 53

RESULT 6
US-09-139-600-60
; Sequence 60, Application US/09139600
; Patent No. 6432628
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHOD OF USE
; FILE REFERENCE: 480140.434
; CURRENT APPLICATION NUMBER: US/09/139,600
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 60
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-60

Query Match
Best Local Similarity 41.9%; Score 204; DB 4; Length 53;
Matches 36; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 3 VVWIKDSPTIPTYTDALHVSTVEGYIAYRHDKSGSCFIQTLVDVFTKRKHILELL 53
DB 3 VAVLKNPQSIPTIPTYTDALHVSTVEGYIAYRHDKSGSCFIQTLVDVFTKRKHILELL 53

RESULT 7
US-09-187-789-7
; Sequence 7, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
```

APPLICANT: Fernandez-Alnemir, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 230
TYPE: PRT
ORGANISM: Homo sapien
US-09-187-789-7

Query Match
Best Local Similarity 100.0%; Pred. No. 9.1e-11;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 EIVMTIKDSPQITPTTDAIHVYSTVEG 28
147 EIVMTIKDSPQITPTTDAIHVYSTVEG 174

RESULT 8
US-08-394-189B-6
Sequence 6, Application US/08394189B
Patent No. 562301
GENERAL INFORMATION:
APPLICANT: Horvitz, Robert
APPLICANT: Yuan, Junying
APPLICANT: Shaham, Shai
TITLE OF INVENTION: RELATEDNESS OF HUMAN INTERLEUKIN-1
TITLE OF INVENTION: BETA CONVERTASE GENE TO A C. ELEGANS CELL DEATH
TITLE OF INVENTION: GENE, INHIBITORY PORTIONS OF THESE GENES AND...
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Filing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,189B
FILING DATE: 24-FEB-2005
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/282,211
FILING DATE: 12-JUL-1994
APPLICATION NUMBER: 07/984,182
FILING DATE: 20-NOV-1992
APPLICATION NUMBER: 07/897,788
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bleker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 01997/211001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-394-189B-6

Query Match
Best Local Similarity 25.4%; Score 123.5; DB 2; Length 479;
Matches 29; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

Db 14 PPTTDAIHVSTVEGIAYRHQKSCFIQTIVDFT--KRGHILLETVEYTRMAEAE 71
384 PSQADILIAVATTAQYVSRNSRGSWFIOAVCEVFSJHAKMDVVELLTVNKKVACGF 443

Db 72 LVQEG-KARKTNPEIQTIRKRLY 94
444 QTSQANILIKQMPBLTSLRLLKKFY 467

RESULT 9
US-08-258-287B-37
Sequence 37, Application US/08258287B
Patent No. 6083735
GENERAL INFORMATION:
APPLICANT: Yuan, Junying
APPLICANT: Miura, Masayuki
TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,287B
FILING DATE: 10-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/080,850
FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3920001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
TELEX: 248636 SSR
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: both
US-08-258-287B-37

Query Match
Best Local Similarity 25.4%; Score 123.5; DB 3; Length 497;
Matches 29; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

Db 14 PPTTDAIHVSTVEGIAYRHQKSCFIQTIVDFT--KRGHILLETVEYTRMAEAE 71
402 PSQADILIAVATTAQYVSRNSRGSWFIOAVCEVFSJHAKMDVVELLTVNKKVACGF 461

Db 72 LVQEG-KARKTNPEIQTIRKRLY 94
462 QTSQANILIKQMPBLTSLRLLKKFY 485

RESULT 10
US-08-368-704C-37

```
Sequence 37, Application US/08368704C
Patent No. 6087160
GENERAL INFORMATION:
APPLICANT: Yuan, Junying
APPLICANT: Mura, Masayuki
TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,704C
FILING DATE: 4-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,287
FILING DATE: 10-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/080,850
FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3920002
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: both
US-08-368-704C-37

Query Match 25.4%; Score 123.5; DB 3; Length 497;
Best Local Similarity 34.5%; Pred. No. 1e-07;
Matches 29; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

QY 14 PVTYTAHVSTVEGYIARHDOKSCFQTQTVDPFT--KRGHITLLETVTRRABAE 71
DB 402 PQADILIVATTAQYVSRNARSQSWFIQAVCEVPSLAKOMDVLEITVKKVACGF 461
QY 72 LVQEG-KARKTNPEIQSTLRKRLY 94
DB 462 QTSQGNILIKQMPELTSRLTKKFY 485

RESULT 11
US-08-258-287B-36
Sequence 36, Application US/08258287B
Patent No. 6083735
GENERAL INFORMATION:
APPLICANT: Yuan, Junying
APPLICANT: Mura, Masayuki
TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
```

```
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,287B
FILING DATE: 10-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/080,850
FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3920001
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
TYPE: amino acid
TOPOLOGY: both
US-08-258-287B-36

Query Match 25.4%; Score 123.5; DB 3; Length 503;
Best Local Similarity 34.5%; Pred. No. 1e-07;
Matches 29; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

QY 14 PVTYTAHVSTVEGYIARHDOKSCFQTQTVDPFT--KRGHITLLETVTRRABAE 71
DB 408 PQADILIVATTAQYVSRNARSQSWFIQAVCEVPSLAKOMDVLEITVKKVACGF 467
QY 72 LVQEG-KARKTNPEIQSTLRKRLY 94
DB 468 QTSQGNILIKQMPELTSRLTKKFY 491

RESULT 12
US-08-368-704C-36
Sequence 36, Application US/08368704C
Patent No. 6087160
GENERAL INFORMATION:
APPLICANT: Yuan, Junying
APPLICANT: Mura, Masayuki
TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,704C
FILING DATE: 4-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,287
FILING DATE: 10-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/080,850
FILING DATE: 24-JUN-1993
```

```

;
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0609.3920002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; TELEEX: 248636 SSX
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 503 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; US-08-368-704C-36

Query Match      25.4%; Score 123.5; DB 3; Length 503;
Best Local Similarity 34.5%; Pred. No. 1e-07;
Matches 29; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

QY 14 PTYTDALHVSSTVGVIYVRHDKGSCFIQTLVDVET--KRGHILELLETVTRMAEAE 71
DB 408 PSQADMLIAVATTAQYVWRNSARGSWFIQAVCEVFSIHAKMDVDVLELTVNKKVACGF 467
QY 72 LVQEG-KARKTNPEIQSTLRRLY 94
DB 468 QTSQGSNLIKQMPELTSRLKKFY 491

RESULT 13
US-08-394-189B-5
; Sequence 5, Application US/08394189B
; Patent No. 5962301
; GENERAL INFORMATION:
; APPLICANT: Horvitz, Robert
; APPLICANT: Yuan, Junying
; APPLICANT: Shahan, Shai
; TITLE OF INVENTION: RELATEDNESS OF HUMAN INTERLEUKIN-1
; TITLE OF INVENTION: BETA CONVERTASE GENE TO A C. ELBANS CELL DEATH
; TITLE OF INVENTION: GENE, INHIBITORY PORTIONS OF THESE GENES AND...
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESS: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/394,189B
; FILING DATE: 24-FEB-2005
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/282,211
; FILING DATE: 12-JUL-1994
; APPLICATION NUMBER: 07/984,182
; FILING DATE: 20-NOV-1992
; APPLICATION NUMBER: 07/897,788
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 01997/211001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
;
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```

;
; LENGTH: 505 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-394-189B-5

Query Match      25.4%; Score 123.5; DB 2; Length 505;
Best Local Similarity 34.5%; Pred. No. 1e-07;
Matches 29; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

QY 14 PTYTDALHVSSTVGVIYVRHDKGSCFIQTLVDVET--KRGHILELLETVTRMAEAE 71
DB 410 PSQADMLIAVATTAQYVWRNSARGSWFIQAVCEVFSIHAKMDVDVLELTVNKKVACGF 469
QY 72 LVQEG-KARKTNPEIQSTLRRLY 94
DB 470 QTSQGSNLIKQMPELTSRLKKFY 493

RESULT 14
PCT-US93-05701-20
; Sequence 20, Application PC/TUS9305701
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Cloning and Characterization of Cell Death Genes
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESS: Massachusetts Institute of Technology
; STREET: 77 Massachusetts Avenue
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; COMPUTER:
; OPERATING SYSTEM:
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05701
; FILING DATE: 19930614
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 505 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: unsure
; LOCATION: at every Xaa
; PCT-US93-05701-20

Query Match      25.4%; Score 123.5; DB 5; Length 505;
Best Local Similarity 34.5%; Pred. No. 1e-07;
Matches 29; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

QY 14 PTYTDALHVSSTVGVIYVRHDKGSCFIQTLVDVET--KRGHILELLETVTRMAEAE 71
DB 410 PSQADMLIAVATTAQYVWRNSARGSWFIQAVCEVFSIHAKMDVDVLELTVNKKVACGF 469
QY 72 LVQEG-KARKTNPEIQSTLRRLY 94
DB 470 QTSQGSNLIKQMPELTSRLKKFY 493

RESULT 15
PCT-US93-05705-5
; Sequence 5, Application PC/TUS9305705
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Inhibitors of Ced-3 and Related Proteins
;
```

```

; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Massachusetts Institute of Technology
; STREET: 77 Massachusetts Avenue
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05705
; FILING DATE: 19930714
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 505 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: unsure
; LOCATION: at every Xaa
; PCT-US93-05705-5

```

```

Query Match      25.4%; Score 123.5; DB 5; Length 505;
Best Local Similarity 34.5%; Pred. No. 1e-07;
Matches 29; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

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```

QY 14 PPTDNLHVSTVEGYIARHDQSGCFIQLVDVFT--KRGHILELITEVTRMAEAE 71
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 410 PQADMILAIYATTAQYVSWNSARGSWFIQAVCEVSLHAKMDVDVEILTEVKKVACGF 469
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 72 LVQEG-KARKTNPEIQTIRKRLY 94
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Db 470 QTSQGSNIHKQMPILSRLLKKFY 493
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Search completed: July 12, 2004, 13:51:58
 Job time : 8.33058 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 12, 2004, 13:50:22 ; Search time 23.6033 Seconds
(without alignments)
1268.642 Million cell updates/sec

Title: US-10-068-564-5_COPY_147_242
Perfect score: 487
Sequence: 1 EIWVWIKDSPQITPTDALT.....KARKTNPETOSTLRKRLYLQ 96

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1279676 seqs, 311918243 residues
Total number of hits satisfying chosen parameters: 1279676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	487	100.0	214	14	US-10-068-564-9
3	487	100.0	229	9	US-09-764-803A-4
4	487	100.0	241	15	US-10-114-432-36
5	487	100.0	241	15	US-10-114-432-37
6	487	100.0	242	9	US-09-764-803A-24
7	487	100.0	242	9	US-09-845-028-2
8	487	100.0	242	9	US-09-845-028-9
9	487	100.0	242	9	US-09-989-903-5
10	487	100.0	242	10	US-09-851-873-105
11	487	100.0	242	14	US-10-068-564-5
12	487	100.0	242	15	US-10-114-432-3
13	487	100.0	242	15	US-10-114-432-11
14	487	100.0	242	15	US-10-114-432-13
15	487	100.0	242	15	US-10-114-432-15

16	487	100.0	242	15	US-10-114-432-17	Sequence 17, Appl
17	487	100.0	242	15	US-10-114-432-18	Sequence 16, Appl
18	487	100.0	242	15	US-10-114-432-22	Sequence 22, Appl
19	487	100.0	242	15	US-10-114-432-23	Sequence 23, Appl
20	487	100.0	242	15	US-10-114-432-26	Sequence 26, Appl
21	487	100.0	242	15	US-10-114-432-27	Sequence 27, Appl
22	487	100.0	242	15	US-10-114-432-28	Sequence 28, Appl
23	487	100.0	242	15	US-10-114-432-30	Sequence 30, Appl
24	487	100.0	242	15	US-10-114-432-31	Sequence 31, Appl
25	487	100.0	242	15	US-10-114-432-67	Sequence 67, Appl
26	487	100.0	242	15	US-10-114-432-69	Sequence 69, Appl
27	487	100.0	242	15	US-10-114-432-71	Sequence 71, Appl
28	487	100.0	242	15	US-10-114-432-73	Sequence 73, Appl
29	487	100.0	321	15	US-10-114-432-9	Sequence 9, Appl
30	487	100.0	321	15	US-10-114-432-21	Sequence 21, Appl
31	487	100.0	321	15	US-10-114-432-66	Sequence 66, Appl
32	487	100.0	321	15	US-10-114-432-72	Sequence 72, Appl
33	357	73.3	253	15	US-10-114-432-29	Sequence 29, Appl
34	357	73.3	257	9	US-09-764-803A-2	Sequence 2, Appl
35	357	73.3	260	9	US-09-989-903-2	Sequence 2, Appl
36	357	73.3	260	14	US-10-068-564-2	Sequence 2, Appl
37	204	41.9	53	9	US-09-989-903-65	Sequence 65, Appl
38	204	41.9	53	14	US-10-068-564-65	Sequence 65, Appl
39	195	40.0	234	12	US-10-275-107-42	Sequence 42, Appl
40	195	40.0	398	16	US-10-467-042-3	Sequence 34, Appl
41	143	29.4	174	15	US-10-114-432-34	Sequence 3, Appl
42	143	29.4	230	9	US-09-989-903-7	Sequence 7, Appl
43	143	29.4	230	14	US-10-068-564-7	Sequence 5, Appl
44	143	29.4	230	15	US-10-114-432-5	Sequence 19, Appl
45	143	29.4	230	15	US-10-114-432-19	

ALIGNMENTS

RESULT 1
US-09-989-903-9
; Sequence 9, Application US/09989903
; Patent No. US20020146804A1
; GENERAL INFORMATION:
; APPLICANT: Alnemerl, Enad S.
; TITLE OF INVENTION: Fernandez-Alnemrl, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434DI
; CURRENT APPLICATION NUMBER: US/09/989,903
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-989-903-9

Query Match 100.0%; Score 487; DB 9; Length 214;
Best Local Similarity 100.0%; Pred. No. 9.6e-52;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIWVWIKDSPQITPTDALT.....KARKTNPETOSTLRKRLYLQ 60
DB 119 EIWVWIKDSPQITPTDALT.....KARKTNPETOSTLRKRLYLQ 178
QY 61 TEVTRMAEAEIVGEGKARKTNPETOSTLRKRLYLQ 96
DB 179 TEVTRMAEAEIVGEGKARKTNPETOSTLRKRLYLQ 214
RESULT 2
US-10-068-564-9
; Sequence 9, Application US/10068564
; Publication No. US20030040096A1
; GENERAL INFORMATION:

```

; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-1, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C2
; CURRENT APPLICATION NUMBER: US/10/068,564
; CURRENT FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 9
; LENGTH: 214
; TYPE: PRF
; ORGANISM: Homo sapien
US-10-068-564-9

Query Match          100.0%; Score 487; DB 14; Length 214;
Best Local Similarity 100.0%; Pred. No. 9,6e-52;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTIKSPQITPIYTDALHYSTVEGYIAYRHQKSGCFIQTLDVDFTKRKGHTLELL 60
DB 119 EIVMTIKSPQITPIYTDALHYSTVEGYIAYRHQKSGCFIQTLDVDFTKRKGHTLELL 178
61 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYLQ 96
179 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYLQ 214

RESULT 3
US-09-764-803A-4
; Sequence 4, Application US/09764803A
; Patent No. US20020034812A1
; GENERAL INFORMATION:
; APPLICANT: Van de Craen, Marc
; APPLICANT: Declercq, Wim
; APPLICANT: Vandenaebale, Peter
; APPLICANT: Fiers, Walter
; TITLE OF INVENTION: NEW CASPASE HOMOLOGUE
; FILE REFERENCE: 2676-4661US
; CURRENT APPLICATION NUMBER: US/09/764, 803A
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: PCT/EP99/04939
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: EP 98202422.6
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentln version 3.0
; SEQ ID NO 4
; LENGTH: 229
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-764-803A-4

Query Match          100.0%; Score 487; DB 9; Length 229;
Best Local Similarity 100.0%; Pred. No. 1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTIKSPQITPIYTDALHYSTVEGYIAYRHQKSGCFIQTLDVDFTKRKGHTLELL 60
DB 134 EIVMTIKSPQITPIYTDALHYSTVEGYIAYRHQKSGCFIQTLDVDFTKRKGHTLELL 193
61 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYLQ 96
194 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYLQ 229

RESULT 4
US-10-114-432-36
; Sequence 36, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.

```

```

; APPLICANT: Fairs, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-2006.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 241
; TYPE: PRF
; ORGANISM: Homo Sapiens
US-10-114-432-36

Query Match          100.0%; Score 487; DB 15; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTIKSPQITPIYTDALHYSTVEGYIAYRHQKSGCFIQTLDVDFTKRKGHTLELL 60
DB 146 EIVMTIKSPQITPIYTDALHYSTVEGYIAYRHQKSGCFIQTLDVDFTKRKGHTLELL 205
61 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYLQ 96
206 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYLQ 241

RESULT 5
US-10-114-432-37
; Sequence 37, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Fairs, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-2006.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 241
; TYPE: PRF
; ORGANISM: Homo Sapiens
US-10-114-432-37

Query Match          100.0%; Score 487; DB 15; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTIKSPQITPIYTDALHYSTVEGYIAYRHQKSGCFIQTLDVDFTKRKGHTLELL 60
DB 146 EIVMTIKSPQITPIYTDALHYSTVEGYIAYRHQKSGCFIQTLDVDFTKRKGHTLELL 205
61 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYLQ 96
206 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYLQ 241

RESULT 6
US-09-764-803A-24

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; Sequence 24, Application US/09764803A
; Patent No. US20020034812A1
; GENERAL INFORMATION:
; APPLICANT: Van de Craen, Marc
; APPLICANT: Declercq, Wim
; APPLICANT: Vandenabeele, Peter
; APPLICANT: Fiers, Walter
; TITLE OF INVENTION: NEW CASPASE HOMOLOGUE
; FILE REFERENCE: 2676-4661US
; CURRENT APPLICATION NUMBER: US/09/764, 803A
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: PCT/EP99/04939
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: EP 98202422.6
; PRIOR FILING DATE: 1999-07-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc. feature
; OTHER INFORMATION: Description of Artificial Sequence: predicted (genscan program)
; US-09-764-803A-24
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Query Match          100.0%; Score 487; DB 9; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EIVWVTKDSPQTIPTTYTDLAHVYSTVEGYIAVRHDQKSCFIQTLVDVFTKRGHILELL 60
DB 147 EIVWVTKDSPQTIPTTYTDLAHVYSTVEGYIAVRHDQKSCFIQTLVDVFTKRGHILELL 206
QY 61 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYIQ 96
DB 207 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYIQ 242
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RESULT 7
US-09-845-028-2
; Sequence 2, Application US/09845028
; Patent No. US20020081705A1
; GENERAL INFORMATION:
; APPLICANT: Mankovich, John
; TITLE OF INVENTION: HUMAN CASPASE-14 COMPOSITIONS
; FILE REFERENCE: BBI-111
; CURRENT APPLICATION NUMBER: US/09/845, 028
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/199, 962
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-845-028-2
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Query Match          100.0%; Score 487; DB 9; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYIQ 96
DB 207 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYIQ 242
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RESULT 8
US-09-845-028-9
; Sequence 9, Application US/09845028
; Patent No. US20020081705A1
; GENERAL INFORMATION:
; APPLICANT: Mankovich, John
; TITLE OF INVENTION: HUMAN CASPASE-14 COMPOSITIONS
; FILE REFERENCE: BBI-111
; CURRENT APPLICATION NUMBER: US/09/845, 028
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/199, 962
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-845-028-9
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Query Match          100.0%; Score 487; DB 9; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EIVWVTKDSPQTIPTTYTDLAHVYSTVEGYIAVRHDQKSCFIQTLVDVFTKRGHILELL 60
DB 147 EIVWVTKDSPQTIPTTYTDLAHVYSTVEGYIAVRHDQKSCFIQTLVDVFTKRGHILELL 206
QY 61 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYIQ 96
DB 207 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYIQ 242
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RESULT 9
US-09-989-903-5
; Sequence 5, Application US/09989903
; Patent No. US20020146804A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434D1
; CURRENT APPLICATION NUMBER: US/09/989, 903
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-989-903-5
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Query Match          100.0%; Score 487; DB 9; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYIQ 96
DB 207 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYIQ 242
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RESULT 10
US-09-851-873-105
; Sequence 105, Application US/09851873
; Publication No. US20030165488A1
; GENERAL INFORMATION:
; APPLICANT: Kleczien, Rolf F
; APPLICANT: Reardon, Ilene M
```

APPLICANT: Weiland, Katherine L
TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
FILE REFERENCE: 28341/00233
CURRENT APPLICATION NUMBER: US/09/851,873
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 105
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 105
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapiens
US-09-851-873-105

Query Match 100.0%; Score 487; DB 10; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 147 EIVWIKDSPQITPTTDLAHVYSTEVEGYIAVRHDKGSCFIQTLVDVFTKRGHILELL 206
QY 61 TEVTRMAEAEIVQEGKARKTNPEIOSTLRKRLYLQ 96
DB 207 TEVTRMAEAEIVQEGKARKTNPEIOSTLRKRLYLQ 242

RESULT 11
US-10-068-564-5
Sequence 5, Application US/10068564
Publication No. US20030040096A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-12, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434C2
CURRENT APPLICATION NUMBER: US/10/068,564
CURRENT FILING DATE: 2002-02-05
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapiens
US-10-068-564-5

Query Match 100.0%; Score 487; DB 14; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVWIKDSPQITPTTDLAHVYSTEVEGYIAVRHDKGSCFIQTLVDVFTKRGHILELL 60
DB 147 EIVWIKDSPQITPTTDLAHVYSTEVEGYIAVRHDKGSCFIQTLVDVFTKRGHILELL 206
QY 61 TEVTRMAEAEIVQEGKARKTNPEIOSTLRKRLYLQ 96
DB 207 TEVTRMAEAEIVQEGKARKTNPEIOSTLRKRLYLQ 242

RESULT 12
US-10-114-432-3
Sequence 3, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Farris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND

TITLE OF INVENTION: DETECTION OF CANCER
FILE REFERENCE: 51158-20066.00
CURRENT APPLICATION NUMBER: US/10/114,432
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 242
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-114-432-3

Query Match 100.0%; Score 487; DB 15; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVWIKDSPQITPTTDLAHVYSTEVEGYIAVRHDKGSCFIQTLVDVFTKRGHILELL 60
DB 147 EIVWIKDSPQITPTTDLAHVYSTEVEGYIAVRHDKGSCFIQTLVDVFTKRGHILELL 206
QY 61 TEVTRMAEAEIVQEGKARKTNPEIOSTLRKRLYLQ 96
DB 207 TEVTRMAEAEIVQEGKARKTNPEIOSTLRKRLYLQ 242

RESULT 13
US-10-114-432-11
Sequence 11, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Farris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20066.00
CURRENT APPLICATION NUMBER: US/10/114,432
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 242
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-114-432-11

Query Match 100.0%; Score 487; DB 15; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVWIKDSPQITPTTDLAHVYSTEVEGYIAVRHDKGSCFIQTLVDVFTKRGHILELL 60
DB 147 EIVWIKDSPQITPTTDLAHVYSTEVEGYIAVRHDKGSCFIQTLVDVFTKRGHILELL 206
QY 61 TEVTRMAEAEIVQEGKARKTNPEIOSTLRKRLYLQ 96
DB 207 TEVTRMAEAEIVQEGKARKTNPEIOSTLRKRLYLQ 242

RESULT 14
US-10-114-432-13
Sequence 13, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Farris, Mary
APPLICANT: Hubert, Rene S.

```
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-13
```

```
Query Match          100.0%; Score 487; DB 15; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1  EIVWYIKDSPQTIPTYTALAHVYSTVEGYIAYRHQKSCFTQTLVDVFTKRGHILEL 60
DB      147 EIVWYIKDSPQTIPTYTALAHVYSTVEGYIAYRHQKSCFTQTLVDVFTKRGHILEL 206
QY      61  TEVTRMAEALVQEGKARKTNPEIQSTLRKRLYLQ 96
DB      207 TEVTRMAEALVQEGKARKTNPEIQSTLRKRLYLQ 242
```

RESULT 15
US-10-114-432-15

```
; Sequence 15, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Chaillita-Eid, Pia M.
; APPLICANT: Raifano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-15
```

```
Query Match          100.0%; Score 487; DB 15; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1  EIVWYIKDSPQTIPTYTALAHVYSTVEGYIAYRHQKSCFTQTLVDVFTKRGHILEL 60
DB      147 EIVWYIKDSPQTIPTYTALAHVYSTVEGYIAYRHQKSCFTQTLVDVFTKRGHILEL 206
QY      61  TEVTRMAEALVQEGKARKTNPEIQSTLRKRLYLQ 96
DB      207 TEVTRMAEALVQEGKARKTNPEIQSTLRKRLYLQ 242
```

Search completed: July 12, 2004, 14:04:01
Job time : 24.6033 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 12, 2004, 13:44:06 ; Search time 6.94215 Seconds

(without alignments)
1330.191 Million cell updates/sec

Title: US-10-068-564-5_COPY_147_242

Perfect score: 487

Sequence: 1 EIVWIKDSPTPIPTDALT.....KARKTNPETQSTLRKRLYLQ 96

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	length	ID	Description
1	487	100.0	242	2 UC7517	caspace-14/a - hum
2	127.5	26.2	488	2 T13385	hypothetical prote
3	123	25.3	277	2 UC5410	CP32 protein - mo
4	122.5	25.2	503	2 A49429	interleukin-1 beta
5	122	25.1	277	2 S64710	cysteine proteinas
6	115	23.6	536	2 T43633	caspace-related pr
7	109	22.4	277	2 A55315	hypothetical prote
8	105.5	21.7	642	2 T27021	hypothetical prote
9	104	21.4	495	2 T20038	caspace-2 - rat
10	101.5	20.8	452	2 UC6507	hypothetical prote
11	101.5	20.8	826	2 T43638	caspace-related pr
12	99	20.3	454	2 JC7123	caspace-9 long cna
13	98.5	20.2	435	2 A54821	apoptosis regulato
14	98	20.1	416	2 G02635	ICR-LAP6 - human
15	97.5	20.0	139	2 T43642	caspace protein 3
16	97	18.7	394	2 T26968	hypothetical prote
17	86	17.7	212	2 S7437	cysteine proteinas
18	78.5	16.1	505	2 T39520	H+-transporting tw
19	73.5	15.1	526	2 T21811	hypothetical prote
20	71.5	14.7	407	2 UC851	polyketide synthas
21	71.5	14.7	407	2 T17222	Pms protein - huma
22	71.5	14.3	1190	2 S21977	probable DNA polym
23	69.5	14.3	366	2 T03907	valine-cRNA ligase
24	69.5	14.3	1165	2 F71365	hypothetical prote
25	69	14.2	473	2 A70423	udp-glucose 4-epim
26	68	14.0	317	2 A75008	epidermal growth f
27	68	14.0	896	2 S43074	hypothetical prote
28	67.5	13.9	164	2 S56476	

30	67.5	13.9	226	2 T16991	ribonuclease (EC 3
31	67.5	13.9	493	1 S17653	NADH dehydrogenas
32	67	13.8	260	2 D27793	methyl coenzyme M
33	67	13.8	342	2 A37952	probable thyroid h
34	67	13.8	352	2 G71328	probable flagellar
35	67	13.8	411	2 A82566	membrane fusion pr
36	67	13.8	418	1 TXYLTA	thyroid hormone re
37	67	13.8	423	2 F64690	type IIS restricti
38	67	13.8	447	2 T05003	hypothetical prote
39	67	13.8	1599	2 T15854	hypothetical prote
40	66.5	13.7	279	2 A86707	transposase of IS9
41	66.5	13.7	2175	2 A59255	myosin VIIa, long
42	66	13.6	391	2 I51097	thyroid hormone re
43	66	13.6	571	2 S24482	conditioned medium
44	66	13.6	571	2 A42138	conditioned medium
45	65.5	13.4	448	2 E82901	RNA polymerase sig

ALIGNMENTS

RESULT 1

UC7517

caspace-14/a - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

C:Accession: UC7517

R:Beckhart, L.; Ban, J.; Fischer, H.; Techachler, E.

Biochem. Biophys. Res. Commun. 277, 655-659, 2000

A:Title: Caspace-14: Analysis of gene structure and mRNA expression during keratinocyte

A:Reference number: UC7517; MUID:20517231; PMID:11062009

A:Contents: Epidermal keratinocytes

A:Accession: UC7517

A:Molecule type: mRNA

A:Residues: 1-242 <ECK>

A:Cross-references: GB:A097874

C:Comment: This enzyme accumulates during keratinocyte differentiation and is activated

A:Gene: casp-14/a

A:Map position: 19p13.1

A:Introns: 9/3; 59/3; 135/1; 174/1; 208/3

C:Keywords: differentiation

Query Match 100.0%; Score 487; DB 2; Length 242;

Best Local Similarity 100.0%; Pred. No. 3.6e-43;

Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVWIKDSPTPIPTDALTAVSVSEGYIAYRHDKSCFTQTLVDVPTKRKHITL 60

DB 147 EIVWIKDSPTPIPTDALTAVSVSEGYIAYRHDKSCFTQTLVDVPTKRKHITL 206

QY 61 TEVTRMAAEIIVQEGKARKTNPEIQSTLRKRLYLQ 96

DB 207 TEVTRMAAEIIVQEGKARKTNPEIQSTLRKRLYLQ 242

RESULT 2

T13385

hypothetical protein 115C2.9 - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C:Accession: T13385

R:Salles, C.; Valenti, P.; Darlamietsou, A.; Henderson, N.; Campbell, L.; Glover, D.

submitted to the EMBL Data Library, May 1999

A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.

A:Reference number: Z17665

A:Accession: T13385

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-488 <CAR>

A:Cross-references: EMBL:AL031581; NID:e1320978; PID:e1331441; PIDN:CAA20893.1

C:Genetics:

A:Cross-references: FlyBase:FBgn0020381

A:Map position: X
A:Introns: 30/3; 272/3; 393/3; 445/2
A>Note: BG:115C2.9

Query Match 26.2%; Score 127.5; DB 2; Length 488;
Best Local Similarity 37.2%; Pred. No. 1.9e-05;
Matches 32; Conservative 12; Mismatches 27; Indels 15; Gaps 3;

QY 16 YVDALHVSIVTEGYIARHDQKSCFIQTLVDVFTKRKG--HILELITVEYTRMAEELV 73
DB 406 HDIMRAMSTVNGYALRLRTQGSWFTGSLCDALDRSASEHIALDILITVNEVS----- 460

QY 74 QFGKARKTN-----PEIQTSLRKRLY 94
DB 461 ---KKGSGNDESMVNVKSTPRQHY 483

RESULT 3
JCS410
CPP32 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999

C:Accession: JCS410
R:Murakami, T.; Urase, K.; Momoi, M.Y.; Kimura, I.; Momoi, T.
Biochem. Biophys. Res. Commun. 231, 770-774, 1997

A:Title: Specific expression of CPP32 in sensory neurons of mouse embryos and activation
A:Reference number: JCS410; MUID:97224429; PMID:9070890

A:Accession: JCS410
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA

A:Residues: 1-277 <MURK>
A:Cross-references: DDBJ:D86352

A:Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons.

Query Match 25.3%; Score 123; DB 2; Length 277;
Best Local Similarity 39.6%; Pred. No. 3e-05;
Matches 36; Conservative 11; Mismatches 36; Indels 8; Gaps 3;

QY 11 QTIPTTDLAHVSTVEGYIARHDQKSCFIQTLVDVFTKRKGHLE--LITEYTRM 67
DB 185 QKIPVADPLVAYSTAPGYSWRNPKDGSWMFIQSLCSML-KUYAHKLEPMHILITRVNRKV 243

QY 68 A-----EAEIVQEGKARKTNPEIQSTLRKRLY 94
DB 244 ATEPESFSLDSTFHAKQIPICTVSMITKRLY 274

RESULT 4
A49429
Interleukin-1 beta-converting enzyme homolog CED-3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
C:Accession: A49429; T37312

R:Yuan, J.; Shaham, S.; Ledoux, S.; Ellis, H.M.; Horvitz, H.R.
Cell 75, 641-652, 1993
A:Title: The C. elegans cell death gene ced-3 encodes a protein similar to mammalian int

A:Reference number: A49429; MUID:94061982; PMID:8242740
A:Accession: A49429

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-503 <YUA>
A:Cross-references: GB:L29052; NID:96503232; PIDN:AAA27982.2; PID:96503233
A>Note: sequence extracted from NCBI backbone (NCIN:139825, NCBIP:139826)

A:Accession: T37312
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-417, 'R', 419-503 <YU2>
A:Cross-references: EMBL:L29052; PIDN:AAA27982.1
C:Genetics:
A:Gene: ced-3
A:Introns: 45/3; 94/2; 179/1; 289/3; 361/1; 403/3; 483/3

Query Match 25.2%; Score 122.5; DB 2; Length 503;
Best Local Similarity 34.5%; Pred. No. 6.5e-05;
Matches 29; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

QY 14 PTYTDLHVSIVTEGYIARHDQKSCFIQTLVDVFT--KRGHILELITVEYTRMAEELV 71
DB 410 PQADILILAYATTAQYVSWRNKSGSWFIQACEVFSTHAKMDVLELITVEYTRMAEELV 469

QY 72 LVQEG-YARKTNPEIQSTLRKRLY 94
DB 470 QTSQSNILKQMPMTSRLTKRKY 493

RESULT 5
S64710
cysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster

C:Species: Cricetus griseus (Chinese hamster)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C:Accession: S64710; S72395

R:Wang, X.; Zelenski, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.
EMBO J. 15, 1012-1020, 1996
A:Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 during

A:Reference number: S64710; MUID:96183185; PMID:8605870
A:Accession: S64710

A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-277 <MAN>

A:Cross-references: EMBL:U27463
R:Wang, X.
submitted to the EMBL Data Library, May 1995

A:Reference number: S72395
A:Accession: S72395
A:Molecule type: mRNA
A:Residues: 1-79, 'A', 81-146, 'Y', 148-277 <MAN>
A:Cross-references: EMBL:U27463; NID:9124443; PIDN:AA01511.1; PID:91244444
C:Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match 25.1%; Score 122; DB 2; Length 277;
Best Local Similarity 39.6%; Pred. No. 3.8e-05;
Matches 36; Conservative 11; Mismatches 36; Indels 8; Gaps 3;

QY 11 QTIPTTDLAHVSTVEGYIARHDQKSCFIQTLVDVFTKRKGHLE--LITEYTRM 67
DB 185 QKIPVADPLVAYSTAPGYSWRNPKDGSWMFIQSLCSML-KUYAHKLEPMHILITRVNRKV 243

QY 68 A-----EAEIVQEGKARKTNPEIQSTLRKRLY 94
DB 244 ATEPESFSLDSTFHAKQIPICTVSMITKRLY 274

RESULT 6
T43633
caspase-related proteinase 1A (EC 3.4.22.-) - Caenorhabditis elegans

N:Contains: caspase 1B
C:Species: Caenorhabditis elegans
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T43633; T43636

R:Shaham, S.
J. Biol. Chem. 273, 35109-35117, 1998
A:Title: Identification of multiple Caenorhabditis elegans caspases and their potential

A:Reference number: T43633; MUID:96074291; PMID:9857046
A:Accession: T43633

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-536 <SHA>

A:Cross-references: EMBL:AF088285; NID:94063367; PIDN:AAC98292.1; PID:94063368
A:Accession: T43636
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 269-536 <SH2>
A:Cross-references: EMBL:AF088286; NID:94063369; PIDN:AAC98293.1; PID:94063370
C:Genetics:
A:Gene: csp-1

A:Map position: 2

C:Function:

A:Description: probably acts in proteolytic cascades to regulate processes such as progeria

C:Keywords: cysteine proteinase; hydrolase

Query Match

Best Local Similarity 23.6%; Score 115; DB 2; Length 536;

Matches 30; Conservative 23; Mismatches 37; Indels 4; Gaps 3;

QY 3 WVAVIDSPQITPTPT-TDALHVSSTVEGYIAYRHDKGSCFIQTLVDVFTK--RKGHILELLEVTYRMA-E 59

Db 436 LMSRIMGTFTSLNADVIISFTTDDGFTSYRDEAGTWYIKSMCKVFENKSKTMHLIDI 495

QY 60 LTVETRR-MAEALVQEGKARKTNPISQTLRKR 92

Db 496 LLETGRNVYTKYENVQGNVVLKQAPETLSRLTKQ 529

RESULT 7

A:Accession: A55315

cysteine proteinase (EC 3.4.22.-) CPP32 precursor - human

N:Alternate names: cysteine proteinase CPP32

C:Date: 06-Feb-1995 #sequence revision 06-Feb-1995 #text_change 01-Dec-2000

C:Accession: A55315; S58899; I39005

R:Reference: Alnemri, T.; Litwack, G.; Alnemri, E.S.

J. Biol. Chem. 269, 30761-30764, 1994

A:Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elegans

A:Reference number: A55315; MUID:95074098; PMID:7983002

A:Accession: A55315

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-277 <FEER>

A:Cross-references: GB:U13737; NID:9561665; PIDN:AAA65015.1; PID:9561666

A:Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammalian

A:Reference number: S58899; MUID:95319529; PMID:7596430

A:Accession: S58899

A:Molecule type: protein

A:Residues: 29-46;176-189, 'E',191-193 <NIC>

R:Reference: M.; Quan, L.T.; O'Rourke, K.; Denoyers, S.; Zeng, Z.; Beidler, D.R.; Poitrier,

Cell 81, 801-809, 1995

A:Title: Yama/CPP32 beta, a mammalian homolog of CED-3, is a C-ma-inhibitable protease

A:Reference number: A56924; MUID:95292347; PMID:7774019

A:Accession: I39005

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-189, 'E',191-277 <RES>

A:Cross-references: EMBL:U26943; NID:9857568; PIDN:AAA74929.1; PID:9857569

C:Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query Match

Best Local Similarity 22.4%; Score 109; DB 2; Length 277;

Matches 33; Conservative 13; Mismatches 36; Indels 6; Gaps 3;

QY 13 IFVTALHVSSTVEGYIAYRHDKGSCFIQTLVDVFTK--RKGHILELLEVTYRMA-E 69

Db 187 IPDADFLYAKSTAPRYGWRNKGDSWFIQSCAMLYKQYADLERMHLITRNKRVAIE 246

QY 70 AEIVQ--EGKARKTNPISQTLRKR 94

Db 247 FESFSDATFAHAKQIPCIIVSMILTKELY 274

RESULT 8

T27021

hypothetical protein Y48E1B.13 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T27021

R:McMurray, A.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z20299

A:Accession: T27021

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-642 <MIL>

A:Cross-references: EMBL:Z93393; PIDN:CA807698.1; GSPDB:GN00020; CESP:Y48E1B.13

A:Experimental source: clone Y48E1B

C:Genetics:

A:Gene: CESP:Y48E1B.13

A:Map position: 2

A:Introns: 79/3; 122/3; 239/2; 286/3; 333/1; 417/3; 487/1; 589/1; 609/3

Query Match

Best Local Similarity 21.7%; Score 105.5; DB 2; Length 642;

Matches 26; Conservative 20; Mismatches 27; Indels 7; Gaps 3;

QY 15 TYT---DALHVSSTVEGYIAYRHDKGSCFIQTLVDVFTK--RKGHILELLEVTYRMA-E 67

Db 500 TFTSLNADVIISFTTDDGFTSYRDEAGTWYIKSMCKVFENKSKTMHLIDIETGRNVV 559

QY 68 AEALVQEGKARKTNPISQ 87

Db 560 TKENVQGNVVLKQAPETVS 579

RESULT 9

T20038

hypothetical protein C48D1.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T20038

R:Burton, J.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z19214

A:Accession: T20038

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-495 <WIL>

A:Cross-references: EMBL:Z81049; PIDN:CA802848.1; GSPDB:GN00022; CESP:C48D1.2

A:Experimental source: clone C48D1

C:Genetics:

A:Gene: CESP:C48D1.2

A:Map position: 4

A:Introns: 44/3; 93/2; 178/1; 288/3; 360/1; 402/3; 466/1

Query Match

Best Local Similarity 21.4%; Score 104; DB 2; Length 495;

Matches 21; Conservative 16; Mismatches 18; Indels 2; Gaps 1;

QY 14 PVTDALHVSSTVEGYIAYRHDKGSCFIQTLVDVFTK--RKGHILELLEVTYRMA 68

Db 409 PSADILIKYATTAQVSWRNBSRGSMFIQAVCEVSTHAKMDVVELLETVNKKVA 465

RESULT 10

JC6507

caespase-2 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: JC6507

R:Rato, N.; Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.

Gene 202, 127-132, 1997

A:Title: Cloning and expression of the cDNA encoding rat caespase-2.

A:Reference number: JC6507; MUID:98087427; PMID:9427555

A:Accession: JC6507

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-452 <SAT>

A:Cross-references: GB:U77933; NID:92769705; PIDN:AAB96379.1; PID:92769706

Query Match

Best Local Similarity 20.8%; Score 101.5; DB 2; Length 452;

Matches 29; Conservative 21; Mismatches 29; Indels 13; Gaps 3;

QY 13 IPTYTDALHYSTVEGYIARHDQKSCFIQTLVDVFTKR--KGHILELLEVTYRMARA 70
 Db 358 LPTRSDMICGYACLCGNAARNTKRGSMWYTEALQVFSERACDMHADMVKVNALIKE- 416

QY 71 ELVQEGKARKTN-----PEIQSTLRKRLYL 95
 Db 417 ---REGVAPGTEFHRCKEMSEYCYSTLCQQLYL 445

RESULT 11
 T43638
 caspase-related proteinase 2A (EC 3.4.22.-) - Caenorhabditis elegans
 N:Contains: caspase 2B
 C:Species: Caenorhabditis elegans
 C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
 C/Accession: T43638; T43639
 R/Shanam, S.
 J. Biol. Chem. 273, 35109-35117, 1998
 A/Title: Identification of multiple Caenorhabditis elegans caspases and their potential
 A/Reference number: Z22587, MUID:99074291, PMID:9857046
 A/Accession: T43638
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-826 <SHA>
 A/Cross-references: EMBL:AF088288; NID:g4063373; PIDN:AAC98295.1; PID:g4063374
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 564-826 <SH2>
 A/Cross-references: EMBL:AF088289; NID:g4063375; PIDN:AAC98296.1; PID:g4063376
 C/Genetics:
 A/Gene: csp-2
 A/Map position: 4
 C/Keywords: cysteine proteinase; hydrolase

Query Match 20.8%; Score 101.5; DB 2; Length 826;
 Best Local Similarity 32.6%; Pred. No. 0.017;
 Matches 29; Conservative 17; Mismatches 40; Indels 3; Gaps 2;

QY 9 SPQTFITYTDALHYSTVEGYIARHDQKSCFIQTLVDVFTKR--KGHILELLEVTYRMARA 66
 Db 735 SHQTSQQADLLVFSSTPGFLSFDEFTKGTWYICELVYVILIENADTHLADLMETNR 794

QY 67 MAEA-ELVQEGKARKTNPEIQSTLRKRLYL 94
 Db 795 VVEKYEADKRVIVICQAPEFWSRFTKQLP 823

RESULT 12
 JC7123
 caspase-9 long chain - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
 C/Accession: JC7123
 R/Fujita, E.; Ujino, A.; Matsumaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T.
 Biochem. Biophys. Res. Commun. 264, 550-555, 1999
 A/Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9.
 A/Reference number: JC7123; MUID:20001956; PMID:10529400
 A/Accession: JC7123
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-454 <FU>
 A/Cross-references: DBJ:AB019600; NID:g6440941; PID:g6440942

Query Match 20.3%; Score 99; DB 2; Length 454;
 Best Local Similarity 30.8%; Pred. No. 0.016;
 Matches 28; Conservative 18; Mismatches 37; Indels 8; Gaps 2;

QY 8 DSPQTFITYTDALHYSTVEGYIARHDQKSCFIQTLVDVFTKR--KGHILELLEVTYRMARA 65
 Db 368 DAVSSLPSPDILVSYSTPGFVSWRDKKSGSMWYTELTDGILFQWARSDELQSLIRV-- 425

QY 66 RMAEELVQEGKARKTNPEIQSTLRKRLYLQ 96
 Db 426 ---ANAVSEKGTYYKOIPGCFNFLRKLLFPK 452

RESULT 13
 A54821
 apoptosis regulator ICH-1, stimulatory form L - human
 C/Species: Homo sapiens (man)
 C/Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
 C/Accession: A54821
 R/Wang, L.; Mizu, M.; Bergeron, L.; Zhu, H.; Yuan, J.
 Cell 78, 739-750, 1994
 A/Title: Ich-1, an Ice/ced-3-related gene, encodes both positive and negative regulators
 A/Reference number: A54821; MUID:94373811; PMID:8087842
 A/Accession: A54821
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-435 <MAN>
 A/Cross-references: GB:U13021; NID:9537291; PID:9537292
 C/Keywords: alternative splicing; apoptosis

Query Match 20.2%; Score 98.5; DB 2; Length 435;
 Best Local Similarity 30.4%; Pred. No. 0.017;
 Matches 28; Conservative 21; Mismatches 30; Indels 13; Gaps 3;

QY 13 IPTYTDALHYSTVEGYIARHDQKSCFIQTLVDVFTKR--KGHILELLEVTYRMARA 70
 Db 341 LPTRSDMICGYACLCGNAARNTKRGSMWYTEALQVFSERACDMHADMVKVNALIKD- 399

QY 71 ELVQEGKARKTN-----PEIQSTLRKRLYL 95
 Db 400 ---REGVAPGTEFHRCKEMSEYCYSTLCRHLYL 428

RESULT 14
 G02635
 ICE-LAP6 - human
 C/Species: Homo sapiens (man)
 C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
 C/Accession: G02635
 R/Yuan, H.; Orth, K.; Chinaiyan, A.M.; Poirier, G.G.; Froelich, C.J.; He, W.W.; Dixit,
 submitted to the EMBL Data Library, April 1996
 A/Reference number: H01513
 A/Accession: G02635
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-416 <DUA>
 A/Cross-references: EMBL:U56390; NID:g1336026; PIDN:AAC50640.1; PID:g1336027

Query Match 20.1%; Score 98; DB 2; Length 416;
 Best Local Similarity 31.5%; Pred. No. 0.019;
 Matches 28; Conservative 22; Mismatches 35; Indels 4; Gaps 3;

QY 8 DSPQTFITYTDALHYSTVEGYIARHDQKSCFIQTLVDVFTKRKGHILELLEVTYRMARA 67
 Db 330 DAISSLPSPDILVSYSTPGFVSWRDKKSGSMWYTELTDLF-EGWAH-SEDLQSLIRV 387

QY 68 AEAEVQEGKARKTNPEIQSTLRKRLYLQ 96
 Db 388 ANAVSVK--GIKKQMPGCFNFLRKLLFPK 414

RESULT 15
 T43642
 caspase protein 3 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
 C/Accession: T43642
 R/Shanam, S.
 J. Biol. Chem. 273, 35109-35117, 1998
 A/Title: Identification of multiple Caenorhabditis elegans caspases and their potential

A:Reference number: Z22587; MUID:99074291; PMID:9857046
A:Accession: T43642
A:Status: preliminary; translated from GB/EMBL/DDDD
A:Molecule type: mRNA
A:Residues: 1-139 <SHA>
A:Cross-references: EMBL:AF088290; NID:G4063377; PIDD:AAAC98297.1; PID:G4063378
C:Genetics:
A:Gene: csp-3
A:Map position: 1

Query Match	20.0%;	Score 97.5;	DB 2;	Length 139;
Best Local Similarity	31.5%;	Pred. No. 0.0062;		
Matches 28;	Conservative 18;	Mismatches 40;	Indels 3;	Gaps 2;

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QY 9 SQQIPRYDADLHVSTVGVIAYRRDDKQSCSIQTLVAVFTK--KRGHILELLEIVTVTR 65
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 43 SHQTSSQADLLVSTSPGFLSPFKQETMDTWIQLGVYIIENADTHIADLLTETNRR 102
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 67 MDEA--ELVQEGAKRKINPEIQSTLRKLY 94
      ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 103 VKEKTEADKRVVVCCKQAPFPMFSRFTKQLP 131
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

Search completed: July 12, 2004, 13:51:03
Job time : 7.94215 secs

Job time : 7.94215 secs

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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:40:11 ; Search time 4.76033 Seconds

(without alignments)
1050.081 Million cell updates/sec

Title: US-10-068-564-5_COPY_147_242

Perfect score: 487
Sequence: 1 EIVWIKDSPTIPTYDAL.....KARKTNPISQTLKRLYLQ 96

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	487	100.0	242	1	ICB6_HUMAN
2	357	73.3	257	1	ICB6_MOUSE
3	123	25.3	277	1	ICB3_MOUSE
4	122.5	25.2	503	1	ICB3_CAEEL
5	120	25.1	277	1	ICB3_CRILLO
6	120	24.6	277	1	ICB3_RAT
7	119.5	24.5	496	1	ICB3_CAEVU
8	114	23.4	303	1	ICB3_MOUSE
9	109	22.4	277	1	ICB3_HUMAN
10	107	22.0	282	1	ICB3_XENLA
11	107	22.0	303	1	ICB7_HUMAN
12	107	22.0	303	1	ICB7_MESAU
13	104.5	21.5	424	1	ICB2_CHICK
14	101.5	20.8	435	1	ICB3_MOUSE
15	101	20.7	276	1	ICB6_MOUSE
16	101	20.7	293	1	ICB6_HUMAN
17	98.5	20.2	435	1	ICB3_HUMAN
18	98	20.1	416	1	ICB3_HUMAN
19	97.5	20.0	299	1	ICB1_SPROF
20	96	19.7	323	1	ICB1_DROME
21	95.5	19.6	479	1	ICB8_HUMAN
22	92	18.9	339	1	ICB1_MOUSE
23	86.5	17.8	521	1	ICB8_HUMAN
24	78.5	16.1	505	1	ATP6_GALST
25	75.5	15.5	480	1	ICB8_MOUSE
26	73.5	15.1	373	1	ICB4_MOUSE
27	71	14.6	874	1	SYV_STRCO
28	69.5	14.3	997	1	DPO1_TREPA
29	69.5	14.3	1165	1	SVV_AQUOE
30	69	14.2	395	1	THB_PAROL
31	69	14.2	2294	1	YC62_ARATH
32	68.5	14.1	1232	1	PM5P_HUMAN
33	68	14.0	418	1	THAB_XENLA

34	68	14.0	896	1	EP15_HUMAN
35	67.5	13.9	197	1	YRGJ_ECOLI
36	67.5	13.9	404	1	ILBC_CANFA
37	67.5	13.9	493	1	NIBM_NEUCR
38	67	13.8	260	1	MCRG_METVA
39	67	13.8	418	1	THA_RANCA
40	66.5	13.7	382	1	ICB8_XENLA
41	66.5	13.7	2215	1	MY7A_HUMAN
42	66	13.6	391	1	THAB_PAROL
43	66	13.6	571	1	CMF_DICTI
44	65	13.3	358	1	FLHB_HELPV
45	65	13.3	373	1	THB_RANCA

ALIGNMENTS

```

RESULT 1
ICB6_HUMAN
ID ICB6_HUMAN STANDARD; PRT; 242 AA.
AC P31944; O95823;
DT 01-JUL-1993 (Rel. 26, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14).
GN CASP14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
ON [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22168928; PubMed=12181750;
RA Pistrutto G., Jost M., Srinivasula S.M., Baffa R., Poyet J.-L.,
RA Kari C., Lazebnik Y., Rodeck U., Alnemri E.S.;
RT "Expression and transcriptional regulation of caspase-14 in simple
RT and complex epithelia.";
RL Cell Death Differ. 9:995-1006(2002).
[2]
RP SEQUENCE OF 68-74; 137-147 AND 154-162.
RC TISSUE=Keratinocytes;
RX MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., Van Damme J., Fuyse M., Gesser B., Celis J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes.";
RL Electrophoresis 13:960-969(1992).
CC -!- FUNCTION: May be involved in the death receptor and granzyme B
CC apoptotic pathways. May function as a downstream signal transducer
CC of cell death.
CC -!- SUBUNIT: May dimerize with large prodomain caspases.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
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CC
CC EMBL; AF097874; AAD16173.1; -.
CC PIR; JC7517; JC7517.
CC HSSP; P29466; IICB.
CC Aarhus/cheat-2DPAGE; 6109; IEF.
CC MEROPS; C14.018; -.
CC Genew; HGNC:1502; CASP14.
CC MIM; 605848; -.
CC GO; GO:0004199; F:caspase activity; TAS.
CC GO; GO:0008544; P:epidermal differentiation; TAS.
CC InterPro; IPR002138; ICE_p10.

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DR InterPro: IPR001309; ICE p20.
DR InterPro: IPR002398; Peptidase C14.
DR Pfam: PF00656; Peptidase C14; 1.
DR PRINTS: PR00376; ILIBENZTME.
DR SMART: SM00115; CASc; 1.
DR PROSITE: PS01121; CASPASE_HIS; FALSE_NEG.
DR PROSITE: PS01122; CASPASE_CYS; FALSE_NEG.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
KM Hydrolyase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 2
FT CHAIN 1 146
FT ACT SITE 147 242
FT ACT SITE 89 89
FT ACT SITE 132 132
SQ SEQUENCE 242 AA; 27679 MW; E539B7E8D808A2 CRC64;

Query Match 100.0%; Score 487; DB 1; Length 242;
Best Local Similarity 100.0%; Pred. No. 3.8e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVWVKDSPTPTPTDPAHYSTVEGYIAYRHDKGSCFIQTLVDVFTKRKGHLELL 60
DB 147 EIVWVKDSPTPTPTDPAHYSTVEGYIAYRHDKGSCFIQTLVDVFTKRKGHLELL 206
QY 61 TEVTRMAEALVQEGKARKTNPFIQSTLRKRLYLQ 96
DB 207 TEVTRMAEALVQEGKARKTNPFIQSTLRKRLYLQ 242

RESULT 2
ICB3 MOUSE STANDARD; PRT; 257 AA.
ID ICB3_MOUSE
AC 089094;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14) (MICE).
GN CASP14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=C57BL/6J;
RA Ahmed M., Stinivasula S.M., Hegde R., Mukattash R.,
RA Fernandes-Alnemri T., Alnemri E.S.;
RT "Identification and characterization of murine caspase-14, a new
member of the caspase family."
RL Cancer Res. 58:5201-5205(1998).
RN 12
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Embryo;
RA MEDLINE=99222069; PubMed=10203698;
RA Van de Craen M., Van Looy G., Pype S., Van Criekinge W.,
RA Van den Brande I., Molemans F., Fiers W., Declercq W.,
RA Vandenbeke P.;
RT "Identification of a new caspase homologue: caspase-14."
RL Cell Death Differ. 5:838-846(1998).
RN 13
RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-136.
RC MEDLINE=9909076; PubMed=9792675;
RA Hu S., Snipas S.J., Vincenz C., Salvesen G., Dixit V.M.;
RT "Caspase-14 is a novel developmentally regulated protease."
RL J. Biol. Chem. 273:29648-29653(1998).
CC -1- FUNCTION: Seems to be involved in the death receptor and granzyme
transducer of cell death. May play a role in ontogenesis and skin
physiology.
CC -1- SUBUNIT: May dimerize with large prodomain caspases.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
```

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CC -1- TISSUE SPECIFICITY: Embryo, adult liver and less in adult brain
and kidney.
CC -1- PTM: CLEAVAGE BY GRANZYME B, CASPASE-8 AND -10 GENERATES THE
TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
PROPEPASE.
CC -1- SIMILARITY: Belongs to peptidase family C14.
-----
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-----
DR EMBL: AF092997; AAC63364.1; -.
DR EMBL: AJ007750; CAA07678.1; -.
DR HSSP: P29466; 1ICE.
DR MEROPS: C14.018; -.
DR MGD: MGI:1335092; Casp14.
DR GO: GO:0006917; P:induction of apoptosis; IDA.
DR InterPro: IPR002138; ICE p10.
DR InterPro: IPR001309; ICE p20.
DR InterPro: IPR002398; Peptidase C14.
DR Pfam: PF00656; Peptidase C14; 1.
DR PRINTS: PR00376; ILIBENZTME.
DR SMART: SM00115; CASc; 1.
DR PROSITE: PS01121; CASPASE_HIS; FALSE_NEG.
DR PROSITE: PS01122; CASPASE_CYS; FALSE_NEG.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
KM Hydrolyase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 7
FT CHAIN 1 8
FT ACT SITE 257 257
FT ACT SITE 93 93
FT ACT SITE 136 136
FT ACT SITE 136 136
FT MUTAGEN C->A: DECREASES IN DEATH-INDUCING
ACTIVITY.
SQ SEQUENCE 257 AA; 29458 MW; A228D88DF8A0EB84 CRC64;

Query Match 73.3%; Score 357; DB 1; Length 257;
Best Local Similarity 70.2%; Pred. No. 2.1e-30;
Matches 66; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 3 VVWVXDSPTPTPTDPAHYSTVEGYIAYRHDKGSCFIQTLVDVFTKRKGHLELLTE 62
DB 164 VAVLKNPQSIPTPTDPAHYSTVEGYIAYRHDKGSCFIQTLVDVFTKRKGHLELLTE 223
QY 63 VTRMAEALVQEGKARKTNPFIQSTLRKRLYLQ 96
DB 224 ITRLMANTEWQEGKARKTNPFIQSTLRKRLYLQ 257

RESULT 3
ICB3 MOUSE STANDARD; PRT; 277 AA.
ID ICB3_MOUSE
AC P70677; O08668; Q90W14;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
protein) (CPP-32) (Caspase-3) (SREBP cleavage activity 1)
DE (SCA-1) (1ICE).
GN CASP3 OR CPP32.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC MEDLINE=96358624; PubMed=8761296;
```

RA Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
 RA Fletcher F.A.;
 RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
 RT a cysteine protease resembling interleukin-1 beta converting enzyme
 RT and CED-3.";
 RL Oncogene 13:749-755(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97224429; PubMed=9070890;
 RA Mukasa T., Urase K., Momoi M.Y., Kimura I., Momoi T.;
 RT "Specific expression of CPP32 in sensory neurons of mouse embryos and
 RT activation of CPP32 in the apoptosis induced by a withdrawal of
 RT NGF.";
 RL Biochem. Biophys. Res. Commun. 231:770-774(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C3H/An;
 RA MEDLINE=97190206; PubMed=9038361;
 RA van de Craen M., Vandenaebelle P., Declercq W., van den Brande I.,
 RA van Loo G., Kolemans F., Schotte P., van Criegelingen W., Beyaert R.,
 RA Fiers W.;
 RT "Characterization of seven murine caspase family members.";
 RL FEBS Lett. 403:61-69(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
 RL Submitted (May-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX STRAIN=FVB/N; TISSUE=Mammary gland;
 RA MEDLINE=22389257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Hopkins R.F., Collins F.S., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Diachenko L., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Stapleton M., Soares M.B., Bonaldi W.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Malley S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy U., Helton B., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schurch A., Schein U.E., Jones S.J.M., Marra W.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE OF 58-277 FROM N.A.
 RA Denis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O.,
 RA Fortin J.-P., Sekaly R.-P.;
 RT "Multiple pathways of apoptosis converging on the CPP32 protease.";
 RL Submitted (Jul-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. At the onset of apoptosis it
 CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
 CC 216-Asp-1-Gly-217 bond. Cleaves and activates steroid regulatory
 CC element binding proteins (SREBPs) between the basic helix-loop-
 CC helix leucine zipper domain and the membrane attachment domain.
 CC Cleaves and activates caspase-6, -7 and -9 (By similarity).
 CC Cleaves IL-1 beta between an Asp and an Ala, releasing the mature
 CC cytokine which is involved in a variety of inflammatory processes.
 CC -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Highest expression in spleen, lung, liver,
 CC kidney and heart. Lower expression in brain, skeletal muscle and
 CC testis.

CC -1- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -----
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 CC -----
 DR EMBL, U54803; AAC52768.1; -.
 DR EMBL, U54802; AAC52768.1; JOINED.
 DR EMBL, U49929; AAC52764.1; -.
 DR EMBL, D86352; BAA21727.1; -.
 DR EMBL, Y13086; CAA73528.1; -.
 DR EMBL, U19522; AAC53196.1; -.
 DR EMBL, BC038825; AAH38825.2; -.
 DR EMBL, U63720; AAD09504.1; -.
 DR PIR, J05410; J05410.
 DR HSRF, P42574; IPRU.
 DR MEROPS, C14.003; -.
 DR MGD, MGI:107739; Casp3.
 DR InterPro, IPR002138; Casp3.
 DR InterPro, IPR001309; ICE p20.
 DR InterPro, IPR002398; Peptidase C14.
 DR Pfam, PF00656; Peptidase C14; I.
 DR PRINTS, PR00376; ILIBCEZYME.
 DR SMART, SM00115; CASC; 1.
 DR PROSITE, PS01122; CASPASE_CYS; 1.
 DR PROSITE, PS01121; CASPASE_HIS; 1.
 DR PROSITE, PS50207; CASPASE_P10; 1.
 DR PROSITE, PS50208; CASPASE_P20; 1.
 KW Hydrolase; Thiol protease; Zymogen; Apoptosis.
 FT PROPEP 1 9
 FT CHAIN 10 28
 FT CHAIN 29 175
 FT ACT_SITE 121 121
 FT ACT_SITE 163 163
 FT CONFLICT 17 17
 FT CONFLICT 51 51
 FT CONFLICT 63 65
 FT CONFLICT 84 84
 FT CONFLICT 95 95
 FT CONFLICT 97 97
 FT CONFLICT 128 128
 FT CONFLICT 135 135
 FT CONFLICT 231 231
 FT CONFLICT 262 262
 SQ SEQUENCE 277 AA; 31474 MW; CE91596F7482605 CRC64;
 Query Match 25.3%; Score 123; DB 1; Length 277;
 Best Local Similarity 39.6%; Pred. No. 1.1e-05;
 Matches 36; Conservative 11; Mismatches 36; Indels 8; Gaps 3;
 QY 11 QITPTYDMLHYSTVEGTAIRHDKGSCFTQTVLVDTTKKGHILE--LITVYTRRM 67
 DB 185 OKIPYRADLVYAVSTVPGVYWNMSXDGSMFIOISCSKL-KYAHKLEPMHILITVRNRY 243
 QY 68 A---EAEIVQEGARKTNPEIQSTLRKRLY 94
 DB 244 ATTFESFSDSTFHAKKQIPCIYVSMILTKELY 274
 RESULT 4
 CED3_CABEL STANDARD; PRT; 503 AA.
 ID CED3_CABEL

AC P42573; P45435; Q9GQ4; Q9NA08;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cell death protein 3 precursor (EC 3.4.22.-).
 GN CED-3 OR C48D1.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A. AND MUTAGENESIS.
 RC STRAIN=Bristol N2;
 RA MEDLINE=94061982; PubMed=8242740;
 RA Yuan J., Shaham S., Ledoux S., Ellis H.M., Horvitz H.R.;
 RT "The C. elegans cell death gene ced-3 encodes a protein similar to
 RT mammalian Interleukin-1 beta-converting enzyme."
 RL Cell 75:641-652(1993).
 RN [2]
 RP REVISION TO 418.
 RA Horvitz H.R.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Burton J.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP REVISIONS.
 RA Durbin R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Acts as a cysteine protease in controlling programmed
 CC cell death by proteolytically activating or inactivating a
 CC substrate protein or proteins, a potential substrate may be ced-4.
 CC Alternatively it might directly cause cell death by
 CC proteolytically cleaving proteins that are crucial for cell
 CC viability.
 CC -!- SUBUNIT: Could be a heterodimer of two subunits derived from the
 CC precursor sequence by a probable autocatalytic mechanism.
 CC -!- DEVELOPMENTAL STAGE: Most abundant during embryogenesis and is
 CC also detected at later stages.
 CC -!- PTM: May be regulated by phosphorylation.
 CC -!- SIMILARITY: Belongs to peptidase family C14.
 CC -!- SIMILARITY: Contains 1 CARD domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L29052; AAA79982.2; -;
 DR EMBL; AF210702; AAG42045.1; -;
 DR EMBL; Z81049; CAB61001.2; -;
 DR PIR; A49429; A49429.
 DR HSSP; P42574; 1CP3.
 DR MOROPS; C14.002; -;
 DR WormPep; C48D1.2; CE29088.
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; ILIBENZYME.
 DR SMART; SM00114; CARD; 1.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS50209; CARD; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.

DR PROSITE; PS50208; CASPASE_P20; 1.
 KW Hydrolyase; Thiol protease; Zymogen; Apoptosis; Phosphorylation.
 FT CHAIN 1 371
 FT
 FT CHAIN 372 503
 FT
 FT DOMAIN 1 91
 FT DOMAIN 107 205
 FT ACT SITE 304 304
 FT ACT SITE 358 358
 FT ACT SITE 358 358
 FT MUTAGEN 27 27
 FT MUTAGEN 65 65
 FT MUTAGEN 360 360
 FT MUTAGEN 449 449
 FT MUTAGEN 466 466
 FT MUTAGEN 483 483
 FT MUTAGEN 486 486
 FT SEQUENCE 503 AA; 56616 MW; 722D5831F94DAA69 CRC64;
 Query Match 25.2%; Score 122.5; DB 1; Length 503;
 Best Local Similarity 34.5%; Pred. No. 2.4e-05;
 Matches 29; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

QY 14 PYTDAHYVSTVEGYIAYRHQKSCFTQTVDFVTKRKHIELTEVRMAAE 71
 Db 410 PQGADLLIYATTAQVSWRNRSARGSWFIQAVGEVSTHAKMDVIELTVAKKVAACG 469
 QY 72 LVDEG-KARKNPEIQSTLRKLY 94
 Db 470 QTSQGSNIKKOMPEMTSRLLKFEY 493

RESULT 5

IC3 CRILLO STANDARD; PRT; 277 AA.
 ID IC3 CRILLO
 AC Q60431;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
 DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
 DE (SCA-1).
 GN CASP3 OR CPP32.
 OS Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 OX NCBI_TaxID=10030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96183185; PubMed=8605870;
 RA Wang X., Zelenksi N.G., Yang J., Sakai J., Brown M.S.,
 RA Goldstein J.L.;
 RT "Cleavage of sterol regulatory element binding proteins (SREBPs) by
 RT CPP32 during apoptosis."
 RL EMBO J. 15:1012-1020(1996).
 CC -!- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. At the onset of apoptosis it
 CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
 CC 216-ASP-Gly-217 bond. Cleaves and activates sterol regulatory
 CC element binding proteins (SREBPs) between the basic helix-loop-
 CC helix leucine zipper domain and the membrane attachment domain.
 CC Cleaves and activates caspase-6, -7 and -9 (By similarity).
 CC -!- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
 CC (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).

CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC -----
DR EMBL; U27463; AAB01511.1; -
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.003; -
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILBCEZYME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KM Hydrolyase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 9
FT PROPEP 10 28 BY SIMILARITY.
FT CHAIN 29 175 APOPAIN P17 SUBUNIT.
FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
FT ACT SITE 121 121 BY SIMILARITY.
FT ACT SITE 163 163 BY SIMILARITY.
SQ SEQUENCE 277 AA; 31612 MW; 0BF8A4590A2828A3 CRC64;

Query Match 25.1%; Score 122; DB 1; Length 277;
Best Local Similarity 39.6%; Pred. No. 1.4e-05;
Matches 36; Conservative 11; Mismatches 36; Indels 8; Gaps 3;

QY 11 QNIPPTDAHYSTVEGYIAVRHODKSCFTQTDVFTYKRGHLE---LITETTRM 67
Db 185 QKIPVADFLVATSPGYSWKPNPDGSMFQSLCSML-KYAHKLEPHILTRVNRKV 243

QY 68 A---EAEIVQEGKAKAKTNPETIOSTLRKLY 94
Db 244 ATEFESFSLDSTFHAKKQIPCIIVSMLTRKLY 274

RESULT 6
ID ICE3 RAT STANDARD; PRT; 277 AA.
AC P55213; P70543; P97699; O62993;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE (SCA-1) (ICP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
DE (SCA-1) (ILICE) (IRP).
GN CASP3 OR CPP32.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96358624; PubMed=8761296;
RA Juan T.S.-C., McNeice I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
RA Fletcher F.A.;
RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
RT a cysteine protease resembling interleukin-1 beta converting enzyme
RT and CED-3.";
RL Oncogene 13:749-755 (1996).
RL [2]
RN SEQUENCE OF 30-241 FROM N.A.
RP TISSUE-Ovary;
RC MEDLINE=96042508; PubMed=7588240;
RX

RA Flaws J.A., Kugu K., Trbovich A.M., Desanti A., Tilly K.I.,
RA Hirschfield A.N., Tilly J.L.;
RT "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and
RT mammalian cell death: dissociation of IRP-induced oligonucleosomal
RT endonuclease activity from morphological apoptosis in granulosa cells
RT of the ovarian follicle.";
RL Endocrinology 136:5042-5053 (1995).
RN [3]
RN SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97184204; PubMed=9030616;
RA N. B., Wu X., Du Y., Su Y., Hamilton-Byrd E., Rockey P.K.,
RA Rostreck P. Jr., Poirier G.G., Paul S.M.;
RT "Cloning and expression of a rat brain interleukin-1beta-converting
RT enzyme (ICE)-related protease (IRP) and its possible role in
RT apoptosis of cultured cerebellar granule neurons.";
RL J. Neurosci. 17:1561-1569 (1997).
RN [4]
RN SEQUENCE OF 1-264 FROM N.A.
RA Yakovlev A.G.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. At the onset of apoptosis it
CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
CC 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory
CC element binding proteins (SREBPs) between the basic helix-loop-
CC helix leucine zipper domain and the membrane attachment domain.
CC Cleaves and activates caspase-6, -7 and -9 (By similarity).
CC -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, LIVER, AND MUSCLE
CC BUT NOT IN KIDNEY OR TESTIS.
CC -1- DEVELOPMENTAL STAGE: Highly expressed in neuron-enriched regions
CC of the developing brain, but down-regulated to low levels in the
CC adult brain.
CC -1- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC PROPEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7, PROPEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
CC VICE VERSA (By similarity).
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U49930; AAC52765.1; -
DR EMBL; U34685; AAC52261.1; -
DR EMBL; U84410; AAC41792.1; -
DR EMBL; U58656; AAB02722.1; -
DR PIR; I67437; I67437.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.003; -
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILBCEZYME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KM Hydrolyase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 9
FT PROPEP 10 28 BY SIMILARITY.
FT CHAIN 29 175 APOPAIN P17 SUBUNIT.

FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
 FT ACT_SITE 121 121 BY SIMILARITY.
 FT ACT_SITE 163 163 BY SIMILARITY.
 FT CONFLICT 25 29 KSMDS -> QVD (IN REF. 4).
 FT CONFLICT 170 170 C -> S (IN REF. 2).
 FT CONFLICT 178 178 T -> A (IN REF. 2).
 FT CONFLICT 182 182 M -> V (IN REF. 2).
 FT CONFLICT 187 187 I -> K (IN REF. 2).
 FT CONFLICT 190 190 E -> G (IN REF. 3).
 FT CONFLICT 199 199 T -> S (IN REF. 2).
 FT CONFLICT 211 211 D -> G (IN REF. 2).
 FT CONFLICT 236 236 T -> I (IN REF. 4).
 FT CONFLICT 245 245 L -> M (IN REF. 3).
 SQ SEQUENCE 277 AA; 31491 MW; ADABF418E2507402 CRC64;

Query Match 24.6%; Score 120; DB 1; Length 277;
 Best Local Similarity 39.6%; Pred. No. 2.2e-05;
 Matches 36; Conservative 10; Mismatches 37; Indels 8; Gaps 3;

QY 11 QTIPTVDALHYSTVEGYIAYRHDKSGCFIOTLVDFTRKRGHILE--LTETVTRM 67
 DB 185 QKIPVEADFLYASTAGYYSWNSRDSWFIQSLC-AMLKLYAHKLEFPHILTRVVKRY 243
 QY 68 A---EAEVQEGKARKTNPFIQSTLRKRLY 94
 DB 244 ATEFESFSLDTEFAKKQIPCIIVSMLTKEY 274

RESULT 7
 CEB3_CAEVU STANDARD; PRT; 496 AA.
 ID CEB3_CAEVU
 AC P45436;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cell death protein 3 precursor (EC 3.4.22.-).
 GN CED-3.
 OS Caenorhabditis vulgaris.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodermidae; Caenorhabditis.
 OX NCBI_TaxID=31233;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94061982; PubMed=8242740;
 RA Yuan J., Shaham S., Ledoux S., Ellis H.M., Horvitz H.R.;
 RT "The C. elegans cell death gene ced-3 encodes a protein similar to
 RT mammalian interleukin-1 beta-converting enzyme.";
 RL Cell 75:641-652(1993).
 CC -1- FUNCTION: Acts as a cysteine protease in controlling programmed
 CC cell death by proteolytically activating or inactivating a
 CC substrate protein or proteins, a potential substrate may be ced-4.
 CC Alternatively it might directly cause cell death by
 CC proteolytically cleaving proteins that are crucial for cell
 CC viability (By similarity).
 CC -1- SUBUNIT: Could be a heterodimer of two subunits derived from the
 CC precursor sequence by a probable autocatalytic mechanism.
 CC -1- PTM: May be regulated by phosphorylation.
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -1- SIMILARITY: Contains 1 CARD domain.
 DR HSSP: P42574; ICP3.
 DR MEROPS: C14.002; -.
 DR InterPro: IPR001315; CARD.
 DR InterPro: IPR001318; ICE_P10.
 DR InterPro: IPR001309; ICE_P20.
 DR InterPro: IPR002398; Peptidase_C14.
 DR Pfam: PF00619; CARD; 1.
 DR Pfam: PF00656; Peptidase_C14; 1.
 DR PRINTS: PR00376; ILIBENZYME.
 DR SMART: SM00114; CARD; 1.
 DR SMART: SM00115; CARD; 1.
 DR PROSITE: PS50209; CARD; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.

DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 KM Hydrolyase; Thiol protease; zymogen, Apoptosis, Phosphorylation.
 FT CHAIN 1 364 CELL DEATH PROTEIN 3 SUBUNIT 1
 FT CHAIN 365 496 (POTENTIAL).
 FT CHAIN 365 496 CELL DEATH PROTEIN 3 SUBUNIT 2
 FT DOMAIN 1 91 (POTENTIAL).
 FT ACT_SITE 308 308 CARD.
 FT ACT_SITE 351 351 BY SIMILARITY.
 SQ SEQUENCE 496 AA; 55945 MW; 58E73C790DC3BD38 CRC64;

Query Match 24.5%; Score 119.5; DB 1; Length 496;
 Best Local Similarity 34.5%; Pred. No. 4.8e-05;
 Matches 29; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

QY 14 PVTVDALHYSTVEGYIAYRHDKSGCFIOTLVDFTRKRGHILELLTEVTRMAEAE 71
 DB 401 PSQADILIRYATYAQVSWNSRDSWFIQAVCEVSTHAKMDVDVLLTEVKKVACGF 460
 QY 72 LVQEG-KARKTNPFIQSTLRKRLY 94
 DB 461 QTSQGANITLKQMPMTSRLTKFY 484

RESULT 8
 ICE7_MOUSE STANDARD; PRT; 303 AA.
 ID ICE7_MOUSE
 AC P97864; 008669;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caspase-7 precursor (EC 3.4.22.-) (ICE2 cysteine protease) (Apoptotic
 DE protease Mch-3).
 GN CASP7 OR MCH3 OR LICE2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=97224489; PubMed=9070923;
 RA Juan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
 RA Copeland N.G., Fletcher F.A.;
 RT "Identification and mapping of Casp7, a cysteine protease resembling
 RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3.";
 RL Genomics 40:86-93(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97236307; PubMed=9125129;
 RA Mukasa T., Khoroku Y., Tsukahara T., Momoi M.Y., Kimura I.,
 RA Momoi T.;
 RT "Wortmannin enhances CPP32-like activity during neuronal
 RT differentiation of P19 embryonal carcinoma cells induced by retinoic
 RT acid.";
 RL Biochem. Biophys. Res. Commun. 232:192-197(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/An;
 RX MEDLINE=97190206; PubMed=9038361;
 RA van de Craen M., Vandenaebelle P., Declercq W., van den Brande I.,
 RA van loo G., Molemans F., Schotte P., van Criekinge W., Beyaert R.,
 RA Fiers W.;
 RT "Characterization of seven murine caspase family members.";
 RL FEBS Lett. 403:61-69(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Klausner S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. Cleaves and activates steryl
 CC regulatory element binding proteins (SRBPs). Overexpression
 CC promotes programmed cell death (By similarity).
 CC -1- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LUNG, LIVER, AND
 CC KIDNEY. LOW LEVELS IN SPLEEN, SKELETAL MUSCLE, AND TESTIS. NO
 CC EXPRESSION IN THE BRAIN.
 CC -1- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
 CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
 CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -----
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 CC or send an email to license@sb-sib.ch).
 CC -----
 DR EMBL: U67321; AAC53068.1; ALT_INIT.
 DR EMBL: D86353; BAA19730.1; -.
 DR EMBL: Y13086; CAA73530.1; -.
 DR EMBL: BC005428; AAH05428.1; -.
 DR HSSP: P42574; IPAU.
 DR MEROPS: C14.004; -.
 DR MGD: MGI:109383; Casp7.
 DR InterPro: IPR002138; ICE_P10.
 DR InterPro: IPR001309; ICE_P20.
 DR InterPro: IPR002398; Peptidase_C14.
 DR Pfam: PF00656; Peptidase_C14; 1.
 DR PRINTS: PR00376; IL1BCENZME.
 DR SMART: SM00115; CASC; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 KM Hydroxylase; Thiol protease; Zymogen; Apoptosis.
 FT PROPEP 1 23
 FT CHAIN 24 198 CASPASE-7 SUBUNIT P20 (BY SIMILARITY).
 FT PROPEP 199 206 BY SIMILARITY.
 FT CHAIN 207 303 CASPASE-7 SUBUNIT P11 (BY SIMILARITY).
 FT ACT SITE 144 144 BY SIMILARITY.
 FT ACT SITE 186 186 BY SIMILARITY.
 FT CONFLICT 10 11 EL -> DW (IN REF. 2).
 FT CONFLICT 45 45 A -> T (IN REF. 2).
 FT CONFLICT 48 49 VR -> RQ (IN REF. 2).
 SQ SEQUENCE 303 AA; 34060 MW; 7477878B5BDE5F744 CRC64;

Query Match 23.4%; Score 114; DB 1; Length 303;
 Best Local Similarity 36.4%; Pred. No. 0.00011;
 Matches 32; Conservative 12; Mismatches 38; Indels 6; Gaps 2;

OY 13 IPTYDALHYSTVGATAYRHDKSGCFIOTLVDFPK--RKSHILELFEVTRMAEA 70
 DB 213 IPVEDHFLFASTVGVGYTSMRPGKSMFVQALCSILNEKGDLFIQTLIVNDRVARH 272
 OY 71 ELVCEGKAR---KTNPETIOSTLRKRLY 94
 DB 273 PESQSDPRFNEKKQIPCMVSNLTRELY 300
 RESULT 9
 ID IC33 HUMAN STANDARD; PRT: 277 AA.
 AC P42574; Q96AN1; Q96KP2;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
 DE protein) (CPP-32) (Caspase-3) (CASP-3) (SRBP cleavage activity 1)
 DE (SCA-1).
 GN CASP3 OR CPP32.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANT GLU-190.
 RC TISSUE=F-cell;
 RX MEDLINE=95074098; PubMed=7983002;
 RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
 RT "CPP32, a novel human apoptotic protein with homology to
 RT Caenorhabditis elegans cell death protein Ced-3 and mammalian
 RT Interleukin-1 beta-converting enzyme.";
 RL J. Biol. Chem. 269:30761-30764(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95292347; PubMed=7774019;
 RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
 RA Beldier D.R., Poirier G.G., Salvesen G.S., Dixit V.M.;
 RT "Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
 RT protease that cleaves the death substrate poly(ADP-ribose)
 RT polymerase.";
 RL Cell 81:801-809(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Vallette F.M., Oliver J.J.;
 RT "Control of the activation of the procaspase-3 by a sequence located
 RT at the N-terminus of the p17 subunit.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANT GLU-190.
 RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A., AND VARIANT GLU-190.
 RC TISSUE=Lymph;
 RX MEDLINE=92388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,
 RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RN SEQUENCE OF 29-46 AND 175-193. AND FUNCTION.
 RX MEDLINE=95319529; PubMed=7596430;
 RA Nicholson D.W., Ali A., Thornberry N.A., Vailancourt J.P., Ding C.K.,
 RA Gallant M., Gareau Y., Griffitt P.R., Labelle M., Lazebnik Y.A.,
 RA Munday N.A., Raju S.M., Smolton M.E., Yamin T.-T., Li V.L.,
 RA Miller D.K.;
 RT "Identification and inhibition of the ICE/CED-3 protease necessary
 RT for mammalian apoptosis.";
 RL Nature 376:37-43(1995).
 RN [7]
 RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-277.
 RX MEDLINE=96266352; PubMed=8673606;
 RA Rocanda J., Nicholson D.W., Fazil K.M., Gallant M., Gareau Y.,
 RA Labelle M., Peterson E.P., Rasper D.M., Ruel R., Vailancourt J.P.,
 RA Thornberry N.A., Becker J.W.;
 RT "The three-dimensional structure of apopain/CPP32, a key mediator of
 RT apoptosis.";
 RL Nat. Struct. Biol. 3:619-625(1996).
 RN [8]
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.
 RX MEDLINE=97197830; PubMed=9045680;
 RA Mital P.R.E., di Marco S., Krebs J.P., Bai X., Karanewsky D.S.,
 RA Priestle J.P., Tomaselli K.J., Grueter M.G.;
 RT "Structure of recombinant human CPP32 in complex with the
 RT tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone.";
 RL J. Biol. Chem. 272:6539-6547(1997).
 RN [9]
 RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE=20283632; PubMed=10821855;
 RA Lee D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A.,
 RA Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S.,
 RA Levy M.A., Demolif W.E. Jr., Keller P.M., Tomaszek T., Head M.S.,
 RA Ryan M.D., Haltiwanger R.C., Liang P.-H., Tomason C.A., McDevitt P.J.,
 RA Johnson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,
 RA Lark M.W., Nadeau D.P., Silva L.J., Gowen M., Nuttall M.E.;
 RT "Potent and selective nonpeptide inhibitors of caspases 3 and 7
 RT inhibit apoptosis and maintain cell functionality.";
 RL J. Biol. Chem. 275:16007-16014(2000).
 RN [10]
 RN PROCESSING.
 RX MEDLINE=96353838; PubMed=8755496;
 RA Fernandez-Alnemir T., Armstrong R.C., Krebs J., Srinivasula S.M.,
 RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
 RA Litwack G., Alnemir E.S.;
 RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
 RT apoptotic cysteine protease containing two PADD-like domains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
 RN [11]
 RN CLEAVAGE OF HUNTINGTIN.
 RX MEDLINE=9631285; PubMed=8696339;
 RA Goldberg Y.P., Nicholson D.W., Rasper D.W., Kalchman M.A., Koide H.B.,
 RA Graham R.K., Brom M., Kazemi-Safarjani P., Thornberry N.A.,
 RA Vailancourt J.P., Hayden M.R.;
 RT "Cleavage of huntingtin by apopain, a proapoptotic cysteine protease,
 RT is modulated by the polyglutamine tract.";
 RL Nat. Genet. 13:442-449(1996).
 RN [12]
 RN FUNCTION: Involved in the activation cascade of caspases
 RN responsible for apoptosis execution. At the onset of apoptosis it
 RN proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
 RN 216-Asp-|-gly-217 bond. Cleaves and activates steroid regulatory
 RN element binding proteins (SRBPs) between the basic helix-loop-
 RN helix leucine zipper domain and the membrane attachment domain.
 RN Cleaves and activates caspase-6, -7 and -9. Involved in the
 RN cleavage of huntingtin.
 RN [13]
 RN ENZYME REGULATION: Inhibited by isatin sulfonamides.
 RN [14]
 RN SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit.
 RN [15]
 RN SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- TISSUE SPECIFICITY. Highly expressed in lung, spleen, heart, liver
 CC and kidney. Moderate levels in brain and skeletal muscle, and low
 CC in testis. Also found in many cell lines, highest expression in
 CC cells of the immune system.
 CC -1- PM: CLEAVAGE BY GRANTYME-B, APAF-1, CASPASE-6, -8 AND -10
 CC GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
 CC PEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
 CC ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
 CC OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
 CC AND VICE VERSA.
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC
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 CC
 CC EMBL: U13737; AA065015.1; -;
 CC EMBL: U13738; AA060355.1; -;
 CC EMBL: U26943; AA074929.1; -;
 CC EMBL: A013369; CAC88866.1; -;
 CC EMBL: AY219866; AA025654.1; -;
 CC EMBL: BC016926; AA016926.1; -;
 CC PIR: A55315; A55315.
 CC PDB: 1PAU; 07-JUL-97.
 CC PDB: 1CP3; 24-DEC-97.
 CC PDB: 1GFV; 23-JUN-00.
 CC MEROPS: C14.003; -;
 CC Genes: HGNC:1504; CASP3.
 CC
 CC GO: 0004208; F:caspase-3 activity; TAS.
 CC GO: 0008624; P:induction of apoptosis by extracellular sig.; TAS.
 CC GO: 0008629; P:induction of apoptosis by intracellular sig.; TAS.
 CC GO: 0009405; P:apoptosis; TAS.
 CC InterPro: IPR001218; ICF_P10.
 CC InterPro: IPR001398; ICE_P20.
 CC InterPro: IPR002398; Peptidase_C14.
 CC Pfam: PF00656; Peptidase_C14; 1.
 CC PRINTS: PR00376; ILBCEZYME.
 CC SMART: SM00115; CASC; 1.
 CC PROSITE: PS01122; CASPASE_CYS; 1.
 CC PROSITE: PS01121; CASPASE_HIS; 1.
 CC PROSITE: PS0207; CASPASE_P10; 1.
 CC PROSITE: PS0208; CASPASE_P20; 1.
 CC Hydrolase; Thiol protease; Apoptosis; Polymorphism;
 CC 3D-structure.
 CC PROPEP 1 9
 CC PROPP 10 28
 CC CHAIN 29 175
 CC CHAIN 176 277
 CC ACT SITE 121 121
 CC ACT SITE 163 163
 CC VARIANT 190 190
 CC
 CC CONFLICT 31 36
 CC STRAND 36 36
 CC STRAND 43 51
 CC HELIX 57 59
 CC TURN 60 60
 CC TURN 60 60
 CC TURN 65 66
 CC HELIX 67 80
 CC TURN 81 82
 CC
 CC Query Match 22.4%; Score 109; DB 1; Length 277;
 CC Best Local Similarity 37.5%; Pred. No. 0.00032;
 CC Matches 33; Conservative 13; Mismatches 36; Indels 6; Gaps 3;
 CC
 CC 13 IPPTDADLVHVSVEGYIAYRHDQKSCFIQTLVDVFTK--RKGHILLETVEYTRMA-E 69
 CC DB IPVDADFLVAYSTAPGYWNRNSKDGSWFIQSLCAWLKQYADKLEPHMLITRVNRKVAYTE 246

QY 70 ABLVQ---EGKARKTNPEIQTLRKRLY 94
DB 247 FESFSPDATHAKQIPICIVSMULTKELY 274

RESULT 10
ICE3_XENLA STANDARD; PRT; 282 AA.
AC P55866;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Caspase-3)
(CASP-3) (XCP32).
GN CASP3.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97184166; PubMed=9030578;
RA Yaoita Y., Nakajima K.;
RT "Induction of apoptosis and CPP32 expression by thyroid hormone in a
myoblastic cell line derived from tadpole tail";
RL J. Biol. Chem. 272:5122-5127(1997).
CC -1- FUNCTION: Important mediator of apoptosis. At the onset of
apoptosis it proteolytically cleaves poly(ADP-ribose) polymerase
(PARP) at a 216-Asp1-Gly-217 bond (By similarity).
CC -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12)
subunits.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- MISCELLANEOUS: The subunits are derived from the precursor
sequence by a probable autocatalytic mechanism and probably by
other caspases (By similarity).
CC -1- SIMILARITY: Belongs to peptidase family C14.
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or send an email to license@isb-sib.ch).
CC OR send an email to license@isb-sib.ch.
DR EMBL: D89784; BAA14018.1; -
DR HSSP: P42574; 1PAU.
DR MEROPS: C14.003; -
DR InterPro: IPR002138; ICB_p10.
DR InterPro: IPR001309; ICB_p20.
DR InterPro: IPR002398; Peptidase C14.
DR Pfam: PF00656; Peptidase C14; 1.
DR PRINTS: PR00376; IILBCEZYMF.
DR SMART: SM00115; CASG; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS0207; CASPASE_P10; 1.
DR PROSITE: PS0208; CASPASE_P20; 1.
DR Hydroxylase, Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 ?
FT CHAIN ? 186
FT ACT SITE 187 282
FT ACT SITE 131 131
FT ACT SITE 174 174
SQ SEQUENCE 282 AA; 32124 MW; CB390E8980CA877F CRC64;
Query Match 22.0%; Score 107; DB 1; Length 282;
Best Local Similarity 34.1%; Pred. No. 0.00053;
Matches 31; Conservative 15; Mismatches 39; Indels 6; Gaps 3;
QY 7 KDSPTIPIYDADALVYISVSGYIARHDKSGSCFIQTLVDVFTKRKH-ILDLITVTV 64

DB 192 REEIRIPVEADFLYAVSTVPGYCSWRDMOSWPIQSLCKMIKLYGSHLELIQILTCVN 251
QY 65 RMA-EAEIVQEGKARKTNPEIQTLRKRLY 94
DB 252 HMVADLPFTFH---AKQIPCVVSMULTKSFY 279

RESULT 11
ICE7_HUMAN STANDARD; PRT; 303 AA.
AC P55210; Q13364; Q96BA0;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
(ICE-LAP3) (Apoptotic protease Mch-3) (CMH-1).
GN CASP7 OR MCH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=96139498; PubMed=8576161;
RA Duan H., Chinnaiyan A.M., Hudson P.L., Wing J.P., He W.-W.,
RT Dixit V.M.;
RL "ICE-LAP3, a novel mammalian homologue of the Caenorhabditis elegans
cell death protein Ced-3 is activated during Fas- and tumor necrosis
factor-induced apoptosis";
RL J. Biol. Chem. 271:1621-1625 (1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Spleen;
RX MEDLINE=96147144; PubMed=8567622;
RA Lipke J.A., Gu Y., Sarnecki C., Caron P.R., Su M.-S.;
RT "Identification and characterization of CPP32/Mch2 homolog 1, a novel
cysteine protease similar to CPP32";
RL J. Biol. Chem. 271:1825-1828 (1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC TISSUE=T-cell;
RX MEDLINE=96105019; PubMed=8521391;
RA Fernandez-Alnemir T., Takahashi A., Armstrong R.C., Krebs J.,
RA Fritz L.C., Tomaseill G.J., Wang L., Yu Z., Croce C.M., Salvason G.,
RA Farnshaw W.C., Litwack G., Alnemir E.S.;
RT "Mch3, a novel human apoptotic cysteine protease highly related to
CPP32";
RL Cancer Res. 55:6045-6052 (1995).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND ALPHA').
RC TISSUE=Fetal lung, and Fetal spleen;
RX MEDLINE=97224489; PubMed=9070923;
RA Juan T.S.-C., McBriec I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
RT Copeland N.G., Fletcher F.A.;
RT "Identification and mapping of Casp7, a cysteine protease resembling
CPP32 beta, interleukin-1 beta converting enzyme, and CED-3";
RL Genomics 40:86-93 (1997).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Walling S.U.,
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Guarnatone P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.D., Lu X., Gibbs R.A.,

CC Proc. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Cleaves and activates sterol
CC regulatory element binding proteins (SREBPs). Proteolytically
CC cleaves poly(ADP-ribose) polymerase (PARP) at a 216-ASP-Gly-217
CC bond. Overexpression promotes programmed cell death (By
CC similarity).
CC -1- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC CPB2 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 AND THE LARGE SUBUNIT OF CPB2 PROTEASE ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U47332; AAC52595.1; -.
CC DR HSSP: P42574; 1PAU.
CC DR MEROPS: C14.004; -.
CC DR InterPro: IPR002138; ICE_p10.
CC DR InterPro: IPR001309; ICE_p20.
CC DR InterPro: IPR002398; Peptidase_C14.
CC DR Pfam: PF00656; Peptidase_C14; 1.
CC DR PRINTS: PR00376; ILIBCNZYME.
CC DR SMART: SM00115; CASc; 1.
CC DR PROSITE: PS01121; CASPASE_CYS; 1.
CC DR PROSITE: PS01121; CASPASE_HIS; 1.
CC DR PROSITE: PS50207; CASPASE_P10; 1.
CC DR PROSITE: PS50208; CASPASE_P20; 1.
CC KW Hydrolyase; Thiol protease; Zymogen; Apoptosis.
CC FT PROPEP 1 23
CC FT CHAIN 24 198 CASPASE-7 SUBUNIT P20.
CC FT PROPEP 199 206 BY SIMILARITY.
CC FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.
CC FT ACT SITE 144 144 BY SIMILARITY.
CC FT ACT SITE 186 186 BY SIMILARITY.
CC SQ SEQUENCE 303 AA; 34037 MW; EA23356D90584648 CRC64;
Query Match 22.0%; Score 107; DB 1; Length 303;
Best Local Similarity 35.2%; Pred. No. 0.00058;
Matches 31; Conservative 15; Mismatches 36; Indels 6; Gaps 3;
QY 13 IPVTALHYVTEGVIAYRHQKSCFIQTLVDVFTK--RKGHILELTETWRMA-- 68
DB 213 IPEADFLFAVSTVPGVYWRNPKGSMFYQALCSITLDEHKKOLEMQLITRRNDVARR 272
QY 69 -EALVQE-GKARKTNPETOSTLRKLY 94
DB 273 FESQCDPCEKFKQIIPCWVSMTKELY 300
RESULT 13
ICB2_CHICK STANDARD; PRT; 424 AA.
AC 098943;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-
DE 11/15).
GN CASP2 OR ICH1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

CC Gallus.
CC NCBI_TaxID=9031;
CC [1]
CC SEQUENCE FROM N.A. (ISOFORMS ICH-1L AND ICH-1S).
CC STRAIN=White Leghorn; TISSUE=Ovarian granulosa.
CC MEDLINE=97368127; PubMed=9224894;
CC Johnson A.L., Bridgman J.T., Bergeron L., Yuan J.;
CC "Characterization of the avian ICH-1 cDNA and expression of ICH-1L
CC mRNA in the hen ovary.";
CC Gene 192:227-233 (1997).
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Might function by either
CC activating some proteins required for cell death or inactivating
CC proteins necessary for cell survival (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=ICH-1L;
CC IsoId=G98943-1; Sequence=Displayed;
CC Note=Only form found in the ovary;
CC Name=ICH-1S;
CC IsoId=G98943-2; Sequence=VSP_000803, VSP_000804;
CC -1- PTM: Heterodimer of a small and a large subunit (By similarity).
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U64963; AAC29881.1; ALT_INIT.
CC DR HSSP: P42574; 1CP3.
CC DR MEROPS: C14.006; -.
CC DR InterPro: IPR001315; CARD.
CC DR InterPro: IPR002138; ICE_p10.
CC DR InterPro: IPR001309; ICE_p20.
CC DR InterPro: IPR002398; Peptidase_C14.
CC DR Pfam: PF00619; CARD; 1.
CC DR Pfam: PF00656; Peptidase_C14; 1.
CC DR PRINTS: PR00376; ILIBCNZYME.
CC DR SMART: SM00114; CARD; 1.
CC DR SMART: SM00115; CASc; 1.
CC DR PROSITE: PS50209; CARD; 1.
CC DR PROSITE: PS01121; CASPASE_CYS; 1.
CC DR PROSITE: PS01121; CASPASE_HIS; 1.
CC DR PROSITE: PS50207; CASPASE_P10; 1.
CC DR PROSITE: PS50208; CASPASE_P20; 1.
CC KW Hydrolyase; Thiol protease; Apoptosis; Zymogen; Alternative splicing.
CC FT PROPEP 1 140
CC FT CHAIN 141 308 CASPASE-2 SUBUNIT P18 (BY SIMILARITY).
CC FT CHAIN 309 424 CASPASE-2 SUBUNIT P13 (BY SIMILARITY).
CC FT CHAIN 315 424 CASPASE-2 SUBUNIT P12 (BY SIMILARITY).
CC FT DOMAIN 7 36 CARD.
CC FT ACT SITE 248 248 BY SIMILARITY.
CC FT ACT SITE 291 291 BY SIMILARITY.
CC FT VARSPLIC 1 7 Missing (in isoform ICH-1S).
CC FT VARSPLIC 294 424 /FTId=VSP_000803.
CC FT VARSPLIC 294 424 DEDPBGVDQDQKERSDPSQCESDANKERNLRLPTPESD
CC MTCGYAKLKTAMRRTKRGSWYTEATITTFPADSDRTHYA
CC DMVKVNRQIKOREGTPGTEPHRCXMSYCTLCADLYL
CC FPGYVPGK -> GVSQIHHLPLPCCHCICSCMRQYGEWI
CC REMARKGOIPOAVRVMQTRKTKISSCVLHAPI (1n
CC isoform ICH-1S).
CC /FTId=VSP_000804.
CC SQ SEQUENCE 424 AA; 47959 MW; 79281050888B260 CRC64;
Query Match 21.5%; Score 104.5; DB 1; Length 424;
Best Local Similarity 31.5%; Pred. No. 0.0015;
Matches 29; Conservative 21; Mismatches 29; Indels 13; Gaps 3;

```

QY 13 IPTYDALHVSIVGEGYIAYRHDKSGSCFTQTLVDVFTK--RKGHILELLETVTRMAEA 70
DB 329 LPTPSDITCGACLCKGNAAMRNTRGSGWYIEALTITVAEDSRDTHVADMLVKVNAIKQ- 387
QY 71 ELVDEGKARKTN-----PEIOSTLRKRLYL 95
DB 388 ---REGYAPGTEPHRCKEMSEYSTLCQDLYL 416

RESULT 14
ICE6_MOUSE STANDARD; PRT; 435 AA.
AC P29594; 008737;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-2 precursor (BC 3.4.22.-) (CASP-2) (ICH-1 protease) (NEDD2
protein).
GN CASP2 OR ICH1 OR NEDD2 OR NEDD-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=95047319; PubMed=7958843;
RA Kumar S., Kinoshita M., Noda M., Copeland N.G., Jenkins N.A.;
RT "Induction of apoptosis by the mouse Nedd2 gene, which encodes a
RT protein similar to the product of the Caenorhabditis elegans cell
RT death gene ced-3 and the mammalian IL-1 beta-converting enzyme.";
RL Genes Dev. 8:1613-1626(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenaebroeck P., Declercq W., van den Brande I.,
RA van Loo G., Moilemans F., Schotte P., van Crielinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
RN [3]
RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92328780; PubMed=1378265;
RA Kumar S., Tomooka Y., Noda M.;
RT "Identification of a set of genes with developmentally down-regulated
RT expression in the mouse brain.";
RL Biochem. Biophys. Res. Commun. 185:1155-1161(1992).
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Might function by either
CC activating some proteins required for cell death or inactivating
CC proteins necessary for cell survival. May be important in
CC multistep carcinogenesis.
CC -1- SUBUNIT: Heterodimer of a small and a large subunit (by
CC similarity).
CC -1- TISSUE SPECIFICITY: High level expression seen in the embryonic
CC CNS, liver, lung, kidney, small intestine, and hair follicles of
CC vibrissae. Moderate expression seen in the skin, oral mucosa,
CC skeletal muscle, submandibular gland and thymus. In the adult, it
CC is highly expressed in spleen, lung and kidney. Moderately in the
CC brain, heart, testis, liver. Low levels in the thymus, skeletal
CC muscle, ovary and gut.
CC -1- DEVELOPMENTAL STAGE: During embryonic development is highly
CC expressed in several types of mouse tissue undergoing high rates
CC of programmed cell death such as central nervous system and
CC kidney.
CC -1- PTM: THE NATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
CC THAT OF OTHER CASPASES (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -1- SIMILARITY: Contains 1 CARD domain.
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL, D28492; BA02876.1; ALT_INIT.
DR EMBL, Y13085; CA073527.1; ALT_INIT.
DR HSSP; P42574; ICP3.
DR MEROPS; C14.006; -.
DR MGD; MGI:97295; Casp2.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR HydroLase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 152
FT CHAIN 153 435
FT CHAIN 317 435
FT CHAIN 331 435
FT DOMAIN 15 103
FT ACT_SITE 260 260
FT ACT_SITE 303 303
FT ACT_SITE 303 303
FT NOTAGEN 303 303
FT CONFLICT 71 71
SQ SEQUENCE 435 AA; 4896 MW; 8984B6AA76E7A676 CRC64;

Query Match 20.8%; Score 101.5; DB 1; Length 435;
Best Local Similarity 31.5%; Pred. No. 0.0033;
Matches 29; Conservative 21; Mismatches 29; Indels 13; Gaps 3;

QY 13 IPTYDALHVSIVGEGYIAYRHDKSGSCFTQTLVDVFTK--RKGHILELLETVTRMAEA 70
DB 341 LPTPSDITCGACLCKGNAAMRNTRGSGWYIEALTITVAEDSRDTHVADMLVKVNAIKQ- 399
QY 71 ELVDEGKARKTN-----PEIOSTLRKRLYL 95
DB 400 ---REGYAPGTEPHRCKEMSEYSTLCQDLYL 428

RESULT 15
ICE6_MOUSE STANDARD; PRT; 276 AA.
AC 008738;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-6 precursor (BC 3.4.22.-) (Apoptotic protease Mch-2).
GN CASP6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenaebroeck P., Declercq W., van den Brande I.,
RA van Loo G., Moilemans F., Schotte P., van Crielinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).

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CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Cleaves poly(ADP-ribose)
CC polymerase in vitro, as well as lamin. Overexpression promotes
CC programmed cell death (By similarity).
CC -1- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 11 kDa (p11) subunit
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Highly expressed in lung, liver, kidney,
CC testis, and heart. Lower levels in spleen, skeletal muscle and
CC brain.
CC -1- PTM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE THE TWO ACTIVE
CC SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
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CC -----
CC EMBL: Y13087; CAA73529.1; -.
CC DR HSSP; P42574; 1PAU.
CC DR MEROPS; C14.005; -.
CC DR MED; MG1:1312921; Casp6.
CC DR InterPro; IPR002138; ICE_p10.
CC DR InterPro; IPR001309; ICE_p20.
CC DR InterPro; IPR002398; Peptidase_C14.
CC DR Pfam; PF00656; Peptidase_C14; 1.
CC DR PRINTS; PR00376; TLBCENZME.
CC DR SMART; SM0115; CASC_1.
CC DR PROSITE; PS01122; CASPASE_CYS; 1.
CC DR PROSITE; PS01121; CASPASE_HIS; 1.
CC DR PROSITE; PS50207; CASPASE_P10; 1.
CC DR PROSITE; PS50208; CASPASE_P20; 1.
CC KW Hydrolyase; Thiol protease; Apoptosis; Zymogen.
CC FT PROPEP 1 BY SIMILARITY.
CC FT CHAIN 5 CASPASE-6 SUBUNIT P18 (BY SIMILARITY).
CC FT PROPEP 6 162 BY SIMILARITY.
CC FT CHAIN 177 276 BY SIMILARITY.
CC FT ACT SITE 104 104 CASPASE-6 SUBUNIT P11 (BY SIMILARITY).
CC FT ACT SITE 146 146 BY SIMILARITY.
CC SQ SEQUENCE 276 AA; 5965DB9321126B6C CRC64;
CC -----
Query Match 20.7%; Score 101; DB 1; Length 276;
Best local Similarity 32.0%; Pred. No. 0.0022;
Matches 32; Conservative 16; Mismatches 44; Indels 8; Gaps 3.
CC -----
QY 2 IWMVTKDSDPQITPTTDAIMHYSTVEGYIAYNHDQSGSCFIOTLVDFVTKRGHLL--E 58
DB 171 VTQVDAASVYTLPAQADFLMVCYSVAEGYYSHRETVNGSMYIDGLCEMLA-RYGSLSLEFTE 229
QY 59 LITEVTRMAEKL-----VQESKAKXINPEIOLSTIRKLKY 94
DB 230 LITLVNRYVSOQRVDFCKDPDPAIGKKQVCFPSASLTKLKH 269

```

Search completed: July 12, 2004, 13:48:23
Job time : 5.76033 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:43:31 ; Search time 19.6364 Seconds

(without alignment)
1542.533 Million cell updates/sec

Title: US-10-068-564-5_COPY_147_242

Sequence: 1 ELVWTKDSPTQTPPTDML.....KARKNPETQSTLRRLVYQ 96

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAD:*
17: SP_ARCHAEP:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	141.5	29.1	283	13	093417 gallus galli
2	132	27.1	282	13	098UI8 O98UI8 brachydanio
3	128	26.3	316	5	0817B0 0817B0 geodia cydo
4	128	26.3	426	5	0816Y2 0816Y2 geodia cydo
5	127.5	26.2	470	5	09WSE3 09WSE3 drosophila
6	127.5	26.2	488	5	09UB42 09UB42 drosophila
7	127.5	26.2	510	5	081RY7 081RY7 drosophila
8	126.5	26.0	488	5	076798 076798 drosophila
9	126.5	26.0	494	5	076797 076797 drosophila
10	125	25.7	277	6	08MTC3 08MTC3 cryetolagus
11	123	25.3	189	11	08BNT4 08BNT4 mus musculus
12	123	25.3	317	11	08CHV5 08CHV5 mus musculus
13	122	25.1	277	6	08MK15 08MK15 canis famill
14	121	24.8	277	6	095ND5 095ND5 sus scrofa
15	119.5	24.5	476	13	0918J3 0918J3 brachydanio
16	117	24.0	277	6	08MJUL 08MJUL felis silve

17	115	23.6	268	5	09TZP6 09TZP6 caenorhabdi
18	115	23.6	536	5	018203 018203 caenorhabdi
19	114.5	23.5	289	5	086FL0 086FL0 anopheles s
20	114.5	23.5	417	5	09YU6 09YU6 pristionchu
21	114	23.4	303	11	088550 088550 rattus norv
22	113	23.2	522	4	081UP5 081UP5 homo sapien
23	112.5	23.1	423	13	091B67 091B67 xenopus lae
24	111.5	22.9	280	13	081GM9 081GM9 fuigu rubrip
25	111.5	22.9	280	13	081G42 081G42 fuigu rubrip
26	111	22.8	290	13	081IS8 081IS8 oryzias lat
27	109.5	22.5	318	13	091B65 091B65 xenopus lae
28	109	22.4	280	13	081IS9 081IS9 oryzias lat
29	107	22.0	328	5	081TP3 081TP3 branchiosto
30	107	22.0	383	13	0919L7 0919L7 brachydanio
31	106.5	21.9	326	5	09GV88 09GV88 hydra atten
32	103	21.1	32	11	09D089 09D089 mus musculi
33	102.5	21.0	520	13	091B62 091B62 xenopus lae
34	102	20.9	303	13	091B66 091B66 xenopus lae
35	102	20.9	304	13	093415 093415 gallus galli
36	101.5	20.8	263	5	09TZP5 09TZP5 caenorhabdi
37	101.5	20.8	452	11	08K241 08K241 mus musculi
38	101.5	20.8	452	11	055194 055194 rattus norv
39	101.5	20.8	452	11	08C9H7 08C9H7 mus musculi
40	101.5	20.8	826	5	09Y055 09Y055 caenorhabdi
41	101	20.7	276	11	099M47 099M47 mus musculi
42	101	20.7	454	11	09JHK1 09JHK1 rattus norv
43	100	20.5	277	11	035397 035397 rattus norv
44	100	20.5	293	5	0819V7 0819V7 bombyx mori
45	100	20.5	454	11	09R0T0 09R0T0 mus musculi

ALIGNMENTS

RESULT 1	093417	PRELIMINARY;	PRT;	283 AA.
ID	093417	01-NOV-1998 (TREMBLrel. 08, Created)		
AC	093417	01-NOV-1998 (TREMBLrel. 08, Last sequence update)		
DT	01-NOV-1998	(TREMBLrel. 08, Last sequence update)		
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)		
DE	Caspase-3.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20149872; PubMed=10684799;			
RA	Johnson A.L., Bridgman J.T.;			
RT	"Caspase-3 and -6 expression and enzyme activity in hen granulosa			
RT	cells."			
RL	Biol. Reprod. 62:589-598(2000).			
DR	EMBL; AF083029; AAC32602.1; --			
DR	HSSP; P42574; IPAU.			
DR	MEROPS; C14.003; --			
DR	GO; GO:0030693; F:caspase activity; IEA.			
DR	GO; GO:0006058; P:proteolysis and peptidolysis; IEA.			
DR	InterPro; IPR002338; ICE_P10.			
DR	InterPro; IPR001309; ICE_P20.			
DR	InterPro; IPR002398; Peptidase_C14.			
DR	Pfam; PF00656; Peptidase_C14; 1.			
DR	PRINTS; PR00376; ILIBCENZYME.			
DR	SMART; SM00115; CASc; 1.			
DR	PROSITE; PS01122; CASPASE_CYS; 1.			
DR	PROSITE; PS01121; CASPASE_HIS; 1.			
DR	PROSITE; PS0207; CASPASE_P10; 1.			
DR	PROSITE; PS0208; CASPASE_P20; 1.			
DR	SEQUENCE	283 AA; 31675 MW; 161242DDFDF4DC4F CRC64;		
SQ				
Query Match	29.1%	Score 141.5; DB 13; Length 283;		
Best Local Similarity	40.4%	Pred. No. 2.6e-07;		

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Matches 36; Conservative 15; Mismatches 33; Indels 5; Gaps 2;
QY 11 QTIPTVTDALHYVSTVEGYIAYRHDKGSCFIQTLVDVFTK--RKGHILELLETVTRMA 68
Db 192 QKTPVADPELFYAVSTAPGYGYSWMAEGSWFIQSLCRMKEHARKLEMLQILTRVNRRA 251
QY 69 EAEVY---OEGVARKTNPEIQSTLRKRLY 94
Db 252 EYESGSTROPFNKKQIPICTVSMLTKEFY 280

RESULT 2
Q98UT8 PRELIMINARY; PRT; 282 AA.
AC Q98UT8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DN Caspase-3.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Yabu T., Okazaki T., Yamashita M.;
RT "Molecular Cloning and Gene Expression of Zebrafish Caspase Related to
RT Mammalian Caspase-3."
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB047003; BAB32409.1; -.
DR HSSP; PA2574; IPAT.
DR MEROPS; C14.003; -.
DR ZFIN; ZDB-GENE-011210-1; casp3.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCNZYME.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 282 AA; 31522 MW; 13C3454F5E0932E CRC64;

Query Match 27.1%; Score 132; DB 13; Length 282;
Best Local Similarity 36.8%; Pred. No. 2.8e-06;
Matches 35; Conservative 18; Mismatches 36; Indels 6; Gaps 3;
QY 6 IKDPTIPTYTDALHYVSTVEGYIAYRHDKGSCFIQTLVDVFTK--RKGHILELLETV 63
Db 185 IPRGRRIPEAFVAVSTVPGYSGMRNMTGWSFIQSLCEMWTXGSLLELQIMTRY 244
QY 64 TRRMA---EAEVQEG-KARKTNPEIQSTLRKRLY 94
Db 245 NKKVALDFESTSNMPPGDAKKQIPICTVSMLTKEFY 279

RESULT 3
Q817B0 PRELIMINARY; PRT; 316 AA.
AC Q817B0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DN Caspase 3.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Astrophorida; Geodidae; Geodia.
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OX NCBI_TaxID=6047;
RN [1]
RP SEQUENCE FROM N.A.
RA Wiens M., Saenger H., Krasko A., Perovic S., Mueller W.E.G.;
RT "Caspase-mediated apoptosis in sponges: cloning and function.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ417903; CAD10676.1; -.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCNZYME.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 316 AA; 35319 MW; 33A46BCCE6C3F9B7 CRC64;

Query Match 26.3%; Score 128; DB 5; Length 316;
Best Local Similarity 32.3%; Pred. No. 8.9e-06;
Matches 30; Conservative 23; Mismatches 30; Indels 10; Gaps 3;
QY 9 SPQTIPTYTDALHYVSTVEGYIAYRHDKGSCFIQTLVDVFTK--TKRGHILELLETVTR 66
Db 218 SRALPTPEADFLVAVSTVPGYSGMRNMTGWSFIQSLCEMWTXGSLLELQIMTRY 277
QY 67 MAEAEVQEGKARKTNPEIQ---STLRKRLYIQ 96
Db 278 VA-----YDFQSRGRNRKQIIPAVYTLTKRLTYFR 305

RESULT 4
Q816Y2 PRELIMINARY; PRT; 426 AA.
AC Q816Y2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DN Caspase-3.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Astrophorida; Geodidae; Geodia.
OX NCBI_TaxID=6047;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Eukaryota;
RA Wiens M., Saenger H., Krasko A., Perovic S., Mueller W.E.G.;
RT "Caspase-mediated apoptosis in sponges: cloning and function.";
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ344144; CAC83013.1; -.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCNZYME.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 426 AA; 48024 MW; 713B5EBC82BED0C1 CRC64;

Query Match 26.3%; Score 128; DB 5; Length 426;
Best Local Similarity 32.3%; Pred. No. 1.3e-05;
Matches 30; Conservative 23; Mismatches 30; Indels 10; Gaps 3;
QY 9 SPQTIPTYTDALHYVSTVEGYIAYRHDKGSCFIQTLVDVFTK--TKRGHILELLETVTR 66
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DB      328 SRRLPTDEAFVLAIVTPEVSWRNSEVGSWIFKAFVDMRLASKRHEHMDILTEVNRK 387
QY      67 MAEALVQSGKARKNTPEIO---STRKRLYLQ 96
DB      388 VA-----YDFQSRGRNKQIPAVTMTLTKLYFR 415

RESULT 5
Q9WSE3 PRELIMINARY; PRT; 470 AA.
AC Q9WSE3; 002433;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Caspase-8/-10 homolog (DREDD).
GN DREDD OR DCP2D OR EG:115C2.9 OR CG7486.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RAS V RPII215(C4);
RX MEDLINE=98021435; PubMed=9380701;
RA Inohara N., Koseki T., Hu Y., Chen S., Nunez G.;
RT "CLARP, a death effector domain-containing protein interacts with
RT caspase-8 and regulates apoptosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
[2]

RA Chen P., Rodriguez A., Erskine R., Thach T., Abrams J.M.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF031652; AAC15843.1; -.
DR EMBL; AF070716; AAC31214.1; -.
DR HSSP; Q15806; 10DU.
DR Flybase; FBgn020381; Dredd.
DR GO; GO:0004200; P:signaling (initiator) caspase activity; NAS.
DR GO; GO:0008632; P:apoptotic program; IEP.
DR GO; GO:0006952; P:defense response; IMP.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; I.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 470 AA; 53412 MW; F9CDB4F1B1CED9ED CRC64;

Query Match 26.2%; Score 127.5; DB 5; Length 470;
Best Local Similarity 37.2%; Pred. No. 1.6e-05;
Matches 32; Conservative 12; Mismatches 27; Indels 15; Gaps 3;

QY      16 YTDALHYSTVEGYIAYRHQDQSGCFIQTIVDVFTKRG--HLELLTEVTRMAEALV 73
DB      388 HIDMLRAMSTVNGVYALHTQTGWSFISGLCDAIRRSASEHIDILITVNEVS----- 442
QY      74 QEGKARKTN-----PEIOSTRKRLYL 94
DB      443 ---KKRGSNDSESWVNVKSTRQHY 465

RESULT 6
Q9UB42 PRELIMINARY; PRT; 488 AA.
AC Q9UB42;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Eg115C2.9 protein.
GN DREDD OR EG:115C2.9 OR CG7486.

OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

RN [1]
RP SEQUENCE FROM N.A.
RA Catherine Salles, Philippe Valenti, Areti Darlamtsou,
RA Nadine Henderson, Iorna Campbell, David Glover;
RT "Sequencing the distal X chromosome of Drosophila melanogaster.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
[2]

RA Benos P.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL031581; CAA20893.1; -.
DR PIR; T13385; T13385.
DR HSSP; Q15806; 10DU.
DR Flybase; FBgn020381; Dredd.
DR GO; GO:0004200; P:signaling (initiator) caspase activity; NAS.
DR GO; GO:0008632; P:apoptotic program; IEP.
DR GO; GO:0006952; P:defense response; IMP.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; I.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 488 AA; 55450 MW; 5D444CBD2DFAC06 CRC64;

Query Match 26.2%; Score 127.5; DB 5; Length 488;
Best Local Similarity 37.2%; Pred. No. 1.7e-05;
Matches 32; Conservative 12; Mismatches 27; Indels 15; Gaps 3;

QY      16 YTDALHYSTVEGYIAYRHQDQSGCFIQTIVDVFTKRG--HLELLTEVTRMAEALV 73
DB      406 HIDMLRAMSTVNGVYALHTQTGWSFISGLCDAIRRSASEHIDILITVNEVS----- 460
QY      74 QEGKARKTN-----PEIOSTRKRLYL 94
DB      461 ---KKRGSNDSESWVNVKSTRQHY 483

RESULT 7
Q8IRY7 PRELIMINARY; PRT; 510 AA.
AC Q8IRY7;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CG7486-PA.
GN DREDD OR EG:115C2.9 OR CG7486.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.B., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amandides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen H.X.,
RA Brandon R.C., Rogers Y.H., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,
RA Abail J.F., Agbayani A., An H.J., Andrews-Pfankoch C., Baldwin D.,
RA Baillet R.M., Basu A., Baxendale J., Bayraksaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Fabios B., Delcher A., Deng Z., Mays A.D., Dew I., Diez S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durkin K.J., Evangelista C.C., Ferrara C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glöck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Mei M.H., Ileguam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Koditz C., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matedi B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rheint K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spredling A.C., Stapleton M., Strong R., Sun B.,
RA Svrtkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster." ;
RL Science 287:2185-2195(2000).
[12]
RN SEQUENCE FROM N.A.
RP Celiker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Goegey J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busen D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Gary N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ileguam C., Jalali M., Kruse D., Li P., Matedi B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Paclab J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svrtkas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome." ;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[13]
RN SEQUENCE FROM N.A.
RP Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochink S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Bertan B., Carlson J.W., Celiker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Seearie S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome." ;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[14]
RN SEQUENCE FROM N.A.
RP Adams M.D., Celiker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[15]
RN SEQUENCE FROM N.A.
RP FlyBase;
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
EMBL: AEO03418; AAM09022.1; -.
FLYBase; FBgn0020381; Dredd.
DR GO:0004200; P:signaling (initiator) caspase activity; NAS.
DR GO:0008632; P:apoptotic program; IBP.
DR GO:0006952; P:defense response; IMP.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00656; Peptidase_C14; 1.
PRINTS; PR00376; IL1BCENZTME.
DR PRINTS; PR00376; IL1BCENZTME.
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DR SMART: SM00115; CASc; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
SQ SEQUENCE 510 AA; 57956 MW; 1CEBDB5728DC88A2 CRC64;
Query Match 26.2%; Score 127.5; DB 5; Length 510;
Best Local Similarity 37.2%; Pred. No. 1.8e-05;
Matches 32; Conservative 12; Mismatches 27; Indels 15; Gaps 3;
QY 16 YTDALHYSTVEGYIAYRHDQKSCFIQTLVVFTRKG--HLELLTEVTRMAAEELV 73
DB 428 HMDLRAMSTVNGYALRHTQTGSWFTGSLCDIDRRSASEHIADITLVTEVS----- 482
QY 74 QEGKARKTN-----PEIOSTLRKRLY 94
DB 483 ---KRGSDNESWVNVSTFRQHY 505
RESULT 8
ID 076798 PRELIMINARY; PRT; 488 AA.
AC 076798;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE DREDD isoform gamma.
GN DREDD OR EG:115C2.9 OR CG7486.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen P., Rodriguez A., Brskine R., Thach T., Abrams J.M.;
RT "Dredd, a novel effector of the apoptosis activators Reaper, Grim, and
RL Hid in Drosophila." ;
RL Dev. Biol. 0:0-0(1998).
DR EMBL: AF083895; AAC33118.1; -.
DR HSSP: Q15806; 1QDT.
DR FLYBase: FBgn0020381; Dredd.
DR GO:0004200; P:signaling (initiator) caspase activity; NAS.
DR GO:0008632; P:apoptotic program; IBP.
DR GO:0006952; P:defense response; IMP.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00656; Peptidase_C14; 1.
PRINTS; PR00376; IL1BCENZTME.
DR SMART: SM00115; CASc; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
SQ SEQUENCE 488 AA; 55436 MW; 5D444CBDD2DBF0D6 CRC64;
Query Match 26.0%; Score 126.5; DB 5; Length 488;
Best Local Similarity 37.2%; Pred. No. 2.2e-05;
Matches 32; Conservative 11; Mismatches 28; Indels 15; Gaps 3;
QY 16 YTDALHYSTVEGYIAYRHDQKSCFIQTLVVFTRKG--HLELLTEVTRMAAEELV 73
DB 406 HMDLRAMSTVNGYALRHTQTGSWFTGSLCDIDRRSASEHIADITLVTEVS----- 460
QY 74 QEGKARKTN-----PEIOSTLRKRLY 94
DB 461 ---KRGSDNESWVNVSTFRQHY 483
RESULT 9
ID 076797 PRELIMINARY; PRT; 494 AA.
AC 076797;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
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RESULT 12
Q8CHV5 PRELIMINARY; PRT; 313 AA.
ID Q8CHV5;
AC Q8CHV5;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, last annotation update)
DE Caspase 3, apoptosis related cysteine protease (Fragment).
GN CASP3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RA Strausberg R.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
EMBL; BC038825; AAH38825.1; -.
DR MGD; MGI:107739; Casp3.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCEZYME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROTEASE.
FT NON TER.
RN [1]
SQ SEQUENCE 313 AA; 35174 MW; 96B98A1F04E769FC CRC64;

Query Match 25.3%; Score 123; DB 11; Length 313;
Best Local Similarity 39.6%; Pred. No. 3.1e-05;
Matches 36; Conservative 11; Mismatches 36; Indels 8; Gaps 3;

QY 11 QTIPPTDALHYSTVEGYIAYRHDKGSCFIQTLDVFTKRKGHTLE---LTETVTRM 67
DB 221 QKIPVADFLYASTAPGYTSWRNSKDGSWFIQSLCAAL-KQYVHKLIEPHMILTRVNRKV 279
QY 68 A---EAEIVQEGKARKTNPETSTLRKRLY 94
DB 280 ATEFESFSDSTFHAKKQIPCIYSMITKELY 310

RESULT 13
Q8MK15 PRELIMINARY; PRT; 277 AA.
ID Q8MK15;
AC Q8MK15;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, last annotation update)
DE Caspase-3.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC Sano J.;
RA "canine caspase-3 gene";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AB085580; BAB92862.1; -.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_p10.
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DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCEZYME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 277 AA; 31334 MW; 7094C76D868BDAB9 CRC64;

Query Match 25.1%; Score 122; DB 6; Length 277;
Best Local Similarity 41.8%; Pred. No. 3.5e-05;
Matches 38; Conservative 10; Mismatches 36; Indels 8; Gaps 4;

QY 11 QTIPPTDALHYSTVEGYIAYRHDKGSCFIQTLDVFTKRKGHTLE---LTETVTRM 67
DB 185 QKIPVADFLYASTAPGYTSWRNSKDGSWFIQSLCAAL-KQYVHKLIEPHMILTRVNRKV 243
QY 68 A-EAEIVQEGKA---RKTNPETSTLRKRLY 95
DB 244 ATEFESFSDSAFHKKQIPCIYSMITKELY 275

RESULT 14
Q95ND5 PRELIMINARY; PRT; 277 AA.
ID Q95ND5;
AC Q95ND5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, last annotation update)
DE Caspase-3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21334413; PubMed=11440638;
RA Muneta Y., Shimajima Y., Mori Y.;
RT "Porcine caspase-3: cloning and its activity during apoptosis of
RL J. Interferon Cytokine Res. 21:409-415 (2001).
DR EMBL; AB029345; BAB5544.1; -.
DR MEROPS; C14.003; -.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCEZYME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 277 AA; 31379 MW; 616C0F56141B012B CRC64;

Query Match 24.8%; Score 121; DB 6; Length 277;
Best Local Similarity 41.8%; Pred. No. 4.5e-05;
Matches 38; Conservative 10; Mismatches 35; Indels 8; Gaps 4;

QY 11 QTIPPTDALHYSTVEGYIAYRHDKGSCFIQTLDVFTKRKGHTLE---LTETVTRM 67
DB 185 QKIPVADFLYASTAPGYTSWRNSKDGSWFIQSLCAAL-KQYVHKLIEPHMILTRVNRKV 243
QY 68 A-EAEIVQEGK---ARKTNPETSTLRKRLY 94
DB 244 ATEFESFSDSTFHAKKQIPCIYSMITKELY 274

RESULT 15
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ID	Accession	Protein Name	PTT	AA
Q918J3		PRELIMINARY;		
AC	Q918J3;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, last annotation update)			
DE	Caspase-8.			
GN	CASP8.			
OS	Brachydanio rerio (Zebrafish) (Danio rerio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxId=7955;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20373792; PubMed=10917738;			
RA	Inohara N., Nunez G.;			
RT	"Genes with homology to mammalian apoptosis regulators identified in zebrafish."			
RL	Cell Death Differ. 7:509-510 (2000) .			
DR	EMBL; AF273220; AAF79207.1; --			
DR	HSSP; Q15806; 10DT.			
DR	MEROPS; C14.009; --			
DR	ZFEN: ZDR-GENE-000713-1; casp8.			
DR	GO; GO:0016328; F:apoptosis regulator activity; IEA.			
DR	GO; GO:0030693; F:caspase activity; IEA.			
DR	GO; GO:0006915; F:apoptosis; IEA.			
DR	GO; GO:0006508; F:proteolysis and peptidolysis; IEA.			
DR	InterPro; IPR001875; DED.			
DR	InterPro; IPR002138; ICE_p10.			
DR	InterPro; IPR001309; ICE_p20.			
DR	InterPro; IPR002398; Peptidase_C14.			
DR	Pfam; PF01335; DED; 2.			
DR	Pfam; PF00656; Peptidase_C14; 1.			
DR	PRINTS; PR00376; IL1BCENZYM.			
DR	SMART; SM00115; CASC; 1.			
DR	SMART; SM00031; DED; 2.			
DR	PROSITE; PS01122; CASPASE_CYS; 1.			
DR	PROSITE; PS0207; CASPASE_P10; 1.			
DR	PROSITE; PS0208; CASPASE_P20; 1.			
DR	PROSITE; PS0168; DED; 2.			
SO	SEQUENCE 476 AA; 54890 MW; F09DFE4B3C3C1FB9 CRC64;			

